

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:08:53 ; Search time 186 Seconds
(without alignments)
44.883 Million cell updates/sec

Title: US-10-799-005a-1

Perfect score: 97
Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	614	2 AAW07908	Aaw07908 Pemphigus
2	97	100.0	999	2 AAR30742	Aar30742 Human pem
3	97	100.0	999	5 AAU78054	Aau78054 Human des
4	97	100.0	999	6 ABR48239	Abu48239 Human bla
5	97	100.0	999	6 ABUS5619	Abu5619 Lung canc
6	97	100.0	999	6 ABUS6662	Abu56662 Lung canc
7	97	100.0	999	6 ADA83744	Ada83744 Human DSG
8	97	100.0	999	7 ADM47209	Adm47209 Desmoglei
9	97	100.0	999	7 ADN39004	Adn39004 Cancer/an
10	97	100.0	999	8 ADJ75518	Adj75518 Marker ge
11	97	100.0	999	8 ADN04164	Adn04164 Antipori
12	97	100.0	999	8 ABM81960	Abm81960 Tumour-as
13	97	100.0	1014	4 ABG12435	Abg12435 Novel hum
14	85	87.6	920	8 ADT99519	Adt99519 Mouse des
15	83	85.6	274	4 ABG12434	Abg12434 Novel hum
16	83	85.6	1040	8 ADT99517	Adt99517 Human des
17	83	85.6	1191	4 ABG12436	Abg12436 Novel hum
18	81	83.5	112	3 AAY64603	Aay64603 Nonclassi
19	81	83.5	778	2 AAU15489	Aau15489 Pemphigus
20	81	83.5	1049	5 AAU78052	Aau78052 Human des
21	81	83.5	1049	8 ADQ19903	Adq19903 Human sof
22	81	83.5	1049	8 ADQ14316	Adq14316 Human des
23	81	83.5	1049	8 ADR41698	Adr41698 Human des
24	81	83.5	1049	8 ADP56044	Adp56044 Human PRO

25	81	83.5	1049	9 AEB77778	Aeb77778 Human des
26	81	83.5	1054	8 ADR66714	Adr66714 Human pro
27	81	83.5	1054	8 ADR66372	Adr66372 Human pro
28	80	82.5	920	8 ADT99559	Adt99559 Hypomorph
29	71	73.2	15	2 AAW04843	Aaw04843 Self epit
30	71	73.2	15	2 AAW64815	Aaw64815 Desmoglei
31	71	73.2	15	2 AAW78814	Aaw78814 Desmoglei
32	71	73.2	15	3 AAB33625	Aab33625 MHC class
33	71	73.2	15	4 AAG93721	Aag93721 Human des
34	71	73.2	15	5 AAO17033	Aao17033 Desmoglei
35	71	73.2	15	6 ABUS6577	Abu65577 MHC class
36	71	73.2	15	8 ADQ14318	Adq14318 Human des
37	71	73.2	15	8 ADR41700	Adr41700 Desmoglei
38	71	73.2	15	9 ADS14310	Ady14310 Desmoglei
39	71	73.2	15	9 ADY26173	Ady26173 MHC Class
40	71	73.2	15	9 AEB77864	Aeb77864 Human des
41	71	73.2	113	3 AAY64604	Aay64604 Nonclassi
42	71	73.2	263	2 AAW13010	Aaw13010 Segment o
43	71	73.2	560	2 AAW13009	Aaw13009 Segment o
44	71	73.2	940	4 AAM39436	Aam39436 Human pol
45	71	73.2	1117	5 AAU78053	Aau78053 Human des
46	71	73.2	1117	8 ADR99232	Adr99232 Clone IMA
47	71	73.2	1117	8 ADU06431	Adu06431 Novel bro
48	71	73.2	1118	5 AAE20286	Aae20286 Human lun
49	71	73.2	1120	4 ABG10284	Abg10284 Novel hum
50	71	73.2	1121	4 AAM41222	Aam41222 Human pol
51	67	69.1	15	8 ADT99548	Adt99548 Conserved
52	65	67.0	15	8 ADT99549	Adt99549 Conserved
53	62	63.9	15	8 ADT99550	Adt99550 Conserved
54	52	53.6	747	7 ADD14035	Add14035 Human src
55	52	53.6	761	8 ADP29437	Adp29437 Human sec
56	52	53.6	848	5 ABG79689	Abg79689 Tumour in
57	52	53.6	900	8 ADP26907	Adp26907 Human N-C
58	52	53.6	905	8 ADQ20653	Adq20653 Human sof
59	52	53.6	906	3 AAY70741	Aay70741 Human N-C
60	52	53.6	906	4 ABG14316	Abg14316 Novel hum
61	52	53.6	906	5 ABM81474	Abm81474 Human N-C
62	52	53.6	906	6 ABR58643	Abu58643 Human can
63	52	53.6	906	6 ABR47406	Abu47406 Breast Ca
64	52	53.6	906	7 ADE55478	Ade55478 Human pro
65	52	53.6	906	7 ADE55482	Ade55482 Human pro
66	52	53.6	906	7 ADE55486	Ade55486 Human pro
67	52	53.6	906	7 ADE55490	Ade55490 Human pro
68	52	53.6	906	7 ADN95503	Adn95503 Human BEC
69	52	53.6	906	8 ADR69159	Adr69159 Human N-C
70	52	53.6	906	9 ADY70663	Ady70663 Human nic
71	52	53.6	906	9 ADZ26571	Adz26571 Human N-C
72	49	50.5	906	5 ABM57233	Abm57233 Mouse isc
73	49	50.5	906	7 ABM55488	Ade55488 Rat Prote
74	49	50.5	906	7 ADE55476	Ade55476 Rat Prote
75	49	50.5	906	7 ADE55484	Ade55484 Rat Prote
76	49	50.5	906	7 ADE55480	Ade55480 Rat Prote
77	48	49.5	793	8 ABM84042	Abm84042 Human dia
78	48	49.5	793	8 ABM84043	Abm84043 Human dia
79	48	49.5	807	3 AAY99405	Aay99405 Human PRO
80	48	49.5	807	4 AAB66154	Aab66154 Protein o
81	48	49.5	807	4 AAB87574	Aab87574 Human PRO
82	48	49.5	807	5 AAB83685	Aab83685 Human PRO
83	48	49.5	807	5 ABG95899	Abg95899 Human sec
84	48	49.5	807	5 ADY31928	Ady31928 Novel hum
85	48	49.5	807	6 ABUS0832	Abu0832 Human PRO
86	48	49.5	807	6 ABO33798	Abu033798 Novel hum
87	48	49.5	807	6 ABUS0924	Abu0924 Novel hum
88	48	49.5	807	6 ABO33983	Abu033983 Human sec
89	48	49.5	807	6 ABU72000	Abu72000 Novel hum
90	48	49.5	807	6 ABU71554	Abu71554 Human sec
91	48	49.5	807	6 ABU72335	Abu72335 Human PRO
92	48	49.5	807	6 ABUS1008	Abu91008 Human PRO
93	48	49.5	807	6 ABUS2544	Abu27329 Human sec
94	48	49.5	807	6 ABUS2544	Abu27329 Human sec
95	48	49.5	807	6 ABUS1194	Abu81194 Human sec
96	48	49.5	807	6 ABUS2141	Abu82141 Novel hum
97	48	49.5	807	6 ABO53308	Abu53308 Novel hum

98	48	49.5	807	6	ABU98311	Abu98311	Novel	hum	171	48	49.5	807	7	ADH23960	Adh23960	Novel	hum
99	48	49.5	807	6	ABU98316	Abu98316	Novel	hum	172	48	49.5	807	7	ADG85364	Adg85364	Novel	hum
100	48	49.5	807	6	ABU82523	Abu82523	Novel	hum	173	48	49.5	807	7	ADH24640	Adh24640	Novel	hum
101	48	49.5	807	6	ABU96487	Abu96487	Human	PRO	174	48	49.5	807	7	ADH37496	Adh37496	Human	sec
102	48	49.5	807	6	ABU72157	Abu72157	Human	PRO	175	48	49.5	807	7	ADH02085	Adh02085	Human	PRO
103	48	49.5	807	6	ABU72321	Abu72321	Human	PRO	176	48	49.5	807	7	ADH37666	Adh37666	Human	sec
104	48	49.5	807	6	ADB17155	Adb17155	Human	tra	177	48	49.5	807	7	ADG85704	Adg85704	Novel	hum
105	48	49.5	807	6	ABO44287	Abu44287	Human	sec	178	48	49.5	807	7	ADH24300	Adh24300	Novel	hum
106	48	49.5	807	6	ABO33647	Abu33647	Novel	hum	179	48	49.5	807	7	ADH38594	Adh38594	Novel	hum
107	48	49.5	807	6	ADA19960	Ada19960	Novel	hum	180	48	49.5	807	7	ADG83715	Adg83715	Human	PRO
108	48	49.5	807	6	ADB17343	Adb17343	Human	tra	181	48	49.5	807	7	ADH29523	Adh29523	Novel	hum
109	48	49.5	807	6	ADA20132	Ada20132	Novel	hum	182	48	49.5	807	7	ADH27639	Adh27639	Novel	hum
110	48	49.5	807	6	ABO34215	Abu34215	Human	sec	183	48	49.5	807	7	ADH37836	Adh37836	Human	sec
111	48	49.5	807	6	ABU72449	Abu72449	Human	PRO	184	48	49.5	807	7	ADH38013	Adh38013	Human	sec
112	48	49.5	807	6	ABO34344	Abu34344	Human	sec	185	48	49.5	807	7	ADH57433	Adh57433	Novel	hum
113	48	49.5	807	6	ADA00429	Ada00429	Human	sec	186	48	49.5	807	7	ADH53575	Adh53575	Novel	hum
114	48	49.5	807	7	ABO44500	Abu44500	Human	sec	187	48	49.5	807	7	ADH53745	Adh53745	Novel	hum
115	48	49.5	807	7	ABO33524	Abu33524	Novel	hum	188	48	49.5	807	7	ADH52081	Adh52081	Novel	hum
116	48	49.5	807	7	ABJ72151	Abj72151	Human	mem	189	48	49.5	807	7	ADH49936	Adh49936	Novel	hum
117	48	49.5	807	7	ADB85671	Adb85671	Novel	hum	190	48	49.5	807	7	ADT25446	Adt25446	Novel	hum
118	48	49.5	807	7	ADB83678	Adb83678	Novel	hum	191	48	49.5	807	7	ADH90239	Adh90239	Novel	hum
119	48	49.5	807	7	ADB80784	Adb80784	Novel	hum	192	48	49.5	807	7	ADT25616	Adt25616	Novel	hum
120	48	49.5	807	7	ADB73325	Adb73325	Novel	hum	193	48	49.5	807	7	ADH97790	Adh97790	Novel	hum
121	48	49.5	807	7	ADB78407	Adb78407	Novel	hum	194	48	49.5	807	7	ADH99422	Adh99422	Human	sec
122	48	49.5	807	7	ADB85055	Adb85055	Human	PRO	195	48	49.5	807	7	ADT03638	Adt03638	Novel	hum
123	48	49.5	807	7	ADB78161	Adb78161	Novel	hum	196	48	49.5	807	7	ADT111995	Adt111995	Human	PRO
124	48	49.5	807	7	ADB87227	Adb87227	Novel	hum	197	48	49.5	807	7	ADH90069	Adh90069	Novel	hum
125	48	49.5	807	7	ADB84809	Adb84809	Human	PRO	198	48	49.5	807	7	ADH98470	Adh98470	Novel	hum
126	48	49.5	807	7	ADB68350	Adb68350	Human	PRO	199	48	49.5	807	7	ADT111145	Adt111145	Human	PRO
127	48	49.5	807	7	ADB68157	Adb68157	Human	PRO	200	48	49.5	807	7	ADT111655	Adt111655	Human	PRO
128	48	49.5	807	7	ADB83924	Adb83924	Novel	hum	201	48	49.5	807	7	ADH98300	Adh98300	Novel	hum
129	48	49.5	807	7	ADB73079	Adb73079	Novel	hum	202	48	49.5	807	7	ADH98640	Adh98640	Novel	hum
130	48	49.5	807	7	ADB90974	Adb90974	Novel	hum	203	48	49.5	807	7	ADH98130	Adh98130	Novel	hum
131	48	49.5	807	7	ADC07054	Adc07054	Human	PRO	204	48	49.5	807	7	ADT05118	Adt05118	Novel	hum
132	48	49.5	807	7	ADC18098	Adc18098	Human	PRO	205	48	49.5	807	7	ADT03468	Adt03468	Novel	hum
133	48	49.5	807	7	ADC17233	Adc17233	Mammalian		206	48	49.5	807	7	ADT04863	Adt04863	Novel	hum
134	48	49.5	807	7	ADC14931	Adc14931	Novel	hum	207	48	49.5	807	7	ADH78317	Adh78317	Human	PRO
135	48	49.5	807	7	ADC36917	Adc36917	Human	PRO	208	48	49.5	807	7	ADT19661	Adt19661	Novel	hum
136	48	49.5	807	7	ADC52426	Adc52426	Novel	hum	209	48	49.5	807	7	ADH90409	Adh90409	Novel	hum
137	48	49.5	807	7	ADC21907	Adc21907	Human	PRO	210	48	49.5	807	7	ADT03128	Adt03128	Novel	hum
138	48	49.5	807	7	ADC49938	Adc49938	Novel	hum	211	48	49.5	807	7	ADH77977	Adh77977	Human	PRO
139	48	49.5	807	7	ADC49137	Adc49137	Novel	hum	212	48	49.5	807	7	ADH97960	Adh97960	Novel	hum
140	48	49.5	807	7	ADC49654	Adc49654	Novel	hum	213	48	49.5	807	7	ADT01345	Adt01345	Novel	hum
141	48	49.5	807	7	ADC47515	Adc47515	Novel	hum	214	48	49.5	807	7	ADT02040	Adt02040	Novel	hum
142	48	49.5	807	7	ADC47260	Adc47260	Novel	hum	215	48	49.5	807	7	ADT03298	Adt03298	Novel	hum
143	48	49.5	807	7	ADC78135	Adc78135	Novel	hum	216	48	49.5	807	7	ADT11485	Adt11485	Human	PRO
144	48	49.5	807	7	ADC06370	Adc06370	Novel	hum	217	48	49.5	807	7	ADT02387	Adt02387	Novel	hum
145	48	49.5	807	7	ADC77889	Adc77889	Novel	hum	218	48	49.5	807	7	ADT111825	Adt111825	Human	PRO
146	48	49.5	807	7	ADD50852	Add50852	Novel	hum	219	48	49.5	807	7	ADT05462	Adt05462	Novel	hum
147	48	49.5	807	7	ADD51098	Add51098	Novel	hum	220	48	49.5	807	7	ADH79534	Adh79534	Novel	hum
148	48	49.5	807	7	ADD70744	Add70744	Human	sec	221	48	49.5	807	7	ADT19491	Adt19491	Novel	hum
149	48	49.5	807	7	ADD39821	Add39821	Human	sec	222	48	49.5	807	7	ADT05292	Adt05292	Novel	hum
150	48	49.5	807	7	ADD70267	Add70267	Human	sec	223	48	49.5	807	7	ADH79704	Adh79704	Novel	hum
151	48	49.5	807	7	ADD36102	Add36102	Novel	hum	224	48	49.5	807	7	ADT01530	Adt01530	Novel	hum
152	48	49.5	807	7	ADD38388	Add38388	Human	sec	225	48	49.5	807	7	ADT01700	Adt01700	Novel	hum
153	48	49.5	807	7	ADD39344	Add39344	Human	sec	226	48	49.5	807	7	ADT01870	Adt01870	Novel	hum
154	48	49.5	807	7	ADD50579	Add50579	Human	PRO	227	48	49.5	807	7	ADH79874	Adh79874	Novel	hum
155	48	49.5	807	7	ADD50333	Add50333	Human	PRO	228	48	49.5	807	7	ADT04692	Adt04692	Novel	hum
156	48	49.5	807	7	ADD38867	Add38867	Human	sec	229	48	49.5	807	7	ADT02828	Adt02828	Novel	hum
157	48	49.5	807	7	ADD40298	Add40298	Human	sec	230	48	49.5	807	7	ADH78147	Adh78147	Human	PRO
158	48	49.5	807	7	ADD51344	Add51344	Novel	hum	231	48	49.5	807	7	ADT25786	Adt25786	Novel	hum
159	48	49.5	807	7	ADD50519	Add50519	Human	sec	232	48	49.5	807	7	ADT25956	Adt25956	Novel	hum
160	48	49.5	807	7	ADD20131	Add20131	Human	sec	233	48	49.5	807	7	ADK65468	Adk65468	Novel	hum
161	48	49.5	807	7	ADD50042	Add50042	Human	sec	234	48	49.5	807	7	ADH98810	Adh98810	Novel	hum
162	48	49.5	807	7	ADD21600	Add21600	Human	sec	235	48	49.5	807	7	ADH80051	Adh80051	Novel	hum
163	48	49.5	807	7	ADF30025	Adf30025	Human	sec	236	48	49.5	807	7	ADL93781	Adl93781	Novel	hum
164	48	49.5	807	7	ADF55918	Adf55918	Human	sec	237	48	49.5	807	8	ADC48891	Adc48891	Novel	hum
165	48	49.5	807	7	ADG01103	Adg01103	Novel	hum	238	48	49.5	807	8	ADC52236	Adc52236	Novel	hum
166	48	49.5	807	7	ADG08656	Adg08656	Novel	hum	239	48	49.5	807	8	ADE21062	Adc21062	Novel	hum
167	48	49.5	807	7	ADF95277	Adf95277	Novel	hum	240	48	49.5	807	8	ADE05906	Adc05906	Human	PRO
168	48	49.5	807	7	ADH24130	Adh24130	Novel	hum	241	48	49.5	807	8	ADD75135	Adh75135	Human	PRO
169	48	49.5	807	7	ADH34156	Adh34156	Novel	hum	242	48	49.5	807	8	ADD75881	Adh75881	Novel	hum
170	48	49.5	807	7	ADH29989	Adh29989	Novel	hum	243	48	49.5	807	8	ADD85113	Adh85113	Novel	hum

244	48	49.5	807	8	ADH86939	Novel hum	317	48	49.5	807	8	ADH07692	Novel hum
245	48	49.5	807	8	ADH20816	Novel hum	318	48	49.5	807	8	ADH86214	Novel hum
246	48	49.5	807	8	ADH39113	Novel hum	319	48	49.5	807	8	ADH24810	Novel hum
247	48	49.5	807	8	ADH05660	Human PRO	320	48	49.5	807	8	ADH25858	Novel hum
248	48	49.5	807	8	ADH73645	Human PRO	321	48	49.5	807	8	ADH38424	Novel hum
249	48	49.5	807	8	ADH78485	Novel hum	322	48	49.5	807	8	ADH57263	Novel hum
250	48	49.5	807	8	ADH21308	Novel hum	323	48	49.5	807	8	ADH52250	Novel hum
251	48	49.5	807	8	ADH77423	Novel hum	324	48	49.5	807	8	ADG34184	Novel hum
252	48	49.5	807	8	ADH20570	Novel hum	325	48	49.5	807	8	ADH04548	Human sec
253	48	49.5	807	8	ADH75635	Human PRO	326	48	49.5	807	8	ADH49616	Novel hum
254	48	49.5	807	8	ADH74151	Human PRO	327	48	49.5	807	8	ADH90579	Novel hum
255	48	49.5	807	8	ADH74397	Human PRO	328	48	49.5	807	8	ADH11315	Human PRO
256	48	49.5	807	8	ADH76127	Novel hum	329	48	49.5	807	8	ADH98980	Novel hum
257	48	49.5	807	8	ADH85619	Novel hum	330	48	49.5	807	8	ADH33654	Human PRO
258	48	49.5	807	8	ADH05168	Human PRO	331	48	49.5	807	8	ADH02210	Novel hum
259	48	49.5	807	8	ADH75381	Human PRO	332	48	49.5	807	8	ADH69748	Human PRO
260	48	49.5	807	8	ADH76925	Novel hum	333	48	49.5	807	8	ADH61549	Human sec
261	48	49.5	807	8	ADH86693	Novel hum	334	48	49.5	807	8	ADH90749	Novel hum
262	48	49.5	807	8	ADH78161	Novel hum	335	48	49.5	807	8	ADH29909	Novel hum
263	48	49.5	807	8	ADH77669	Novel hum	336	48	49.5	807	8	ADH98624	Novel hum
264	48	49.5	807	8	ADH77915	Novel hum	337	48	49.5	807	8	ADH98794	Novel hum
265	48	49.5	807	8	ADH85373	Novel hum	338	48	49.5	807	8	ADH78953	Novel hum
266	48	49.5	807	8	ADH73905	Human PRO	339	48	49.5	807	8	ADH9187	Novel hum
267	48	49.5	807	8	ADH74643	Human PRO	340	48	49.5	807	8	ADH99357	Novel hum
268	48	49.5	807	8	ADH77171	Novel hum	341	48	49.5	807	8	ADH98975	Novel hum
269	48	49.5	807	8	ADH85865	Novel hum	342	48	49.5	807	8	ADH79122	Novel hum
270	48	49.5	807	8	ADH05414	Human PRO	343	48	49.5	807	8	ADK00983	Human PRO
271	48	49.5	807	8	ADH74889	Human PRO	344	48	49.5	807	8	ADK14504	Novel hum
272	48	49.5	807	8	ADH96602	Human sec	345	48	49.5	807	8	ADM27306	Novel hum
273	48	49.5	807	8	ADH35913	Human sec	346	48	49.5	807	8	ADM66664	Human PRO
274	48	49.5	807	8	ADH24812	Human sec	347	48	49.5	807	8	ADM80953	Human PRO
275	48	49.5	807	8	ADH29548	Human sec	348	48	49.5	807	8	ADM194748	Human sec
276	48	49.5	807	8	ADH97079	Human sec	349	48	49.5	807	9	ADY77793	Neoplasti
277	48	49.5	807	8	ADG05701	Novel hum	350	48	49.5	839	8	ABM84041	Human dia
278	48	49.5	807	8	ADG27255	Human PRO	351	48	49.5	839	8	ABM84040	Human dia
279	48	49.5	807	8	ADG11318	Novel hum	352	47	48.5	112	8	ADR04198	E malodor
280	48	49.5	807	8	ADG12097	Novel hum	353	47	48.5	317	6	ABU23933	Protein e
281	48	49.5	807	8	ADH94654	Novel hum	354	46	47.4	112	8	ADR04196	E raffin
282	48	49.5	807	8	ADH06750	Human PRO	355	46	47.4	299	6	ABU39292	Protein e
283	48	49.5	807	8	ADH06668	Novel hum	356	45	46.4	85	5	ABP01531	Human ORF
284	48	49.5	807	8	ADH06498	Novel hum	357	45	46.4	619	6	ABR41069	Mouse MAP
285	48	49.5	807	8	ADH88919	Novel hum	358	45	46.4	619	6	ABU63413	Mouse hae
286	48	49.5	807	8	ADH27809	Novel hum	359	45	46.4	619	9	AEF78951	Mouse hae
287	48	49.5	807	8	ADH25150	Novel hum	360	45	46.4	619	9	AEF35100	Mouse hae
288	48	49.5	807	8	ADH33782	Human PRO	361	45	46.4	620	6	ABU63414	Rat haeme
289	48	49.5	807	8	ADH03117	Human sec	362	45	46.4	620	6	ADH78952	Rat haeme
290	48	49.5	807	8	ADH02425	Human PRO	363	45	46.4	620	9	AEF35101	Rat haeme
291	48	49.5	807	8	ADH08032	Novel hum	364	45	46.4	620	9	AEF35101	Rat haeme
292	48	49.5	807	8	ADH69429	Novel hum	365	45	46.4	1321	8	ADM23549	Bacterial
293	48	49.5	807	8	ADH39249	Novel hum	366	44.5	45.9	376	6	ABM67132	Phototrab
294	48	49.5	807	8	ADH04071	Human sec	367	44	45.4	467	7	ADH73293	Stereotr
295	48	49.5	807	8	ADH03594	Human sec	368	44	45.4	913	4	ABG21135	Novel hum
296	48	49.5	807	8	ADH33990	Human PRO	369	44	45.4	935	7	ADC73295	Stereotr
297	48	49.5	807	8	ADH39094	Novel hum	370	44	45.4	1114	8	ADM24247	Bacterial
298	48	49.5	807	8	ADH85534	Novel hum	371	44	45.4	1158	8	ADM24246	Bacterial
299	48	49.5	807	8	ADH06328	Novel hum	372	44	45.4	1732	6	ABP56223	Heliothis
300	48	49.5	807	8	ADH30158	Novel hum	373	43.5	44.8	2380	4	ABB61650	Drosophil
301	48	49.5	807	8	ADH24470	Novel hum	374	43	44.3	325	7	ADB70059	C. neofor
302	48	49.5	807	8	ADG85959	Novel hum	375	43	44.3	859	7	ADM04048	Human pro
303	48	49.5	807	8	ADH07862	Novel hum	376	43	44.3	867	5	ABH33743	Herbicida
304	48	49.5	807	8	ADH85874	Novel hum	377	43	44.3	912	5	ABH81471	Chicken N
305	48	49.5	807	8	ADH39420	Novel hum	378	42.5	43.8	181	8	ADR16473	Human CAV
306	48	49.5	807	8	ADH33612	Human PRO	379	42	43.3	15	8	ADT99554	Conserved
307	48	49.5	807	8	ADH33952	Human PRO	380	42	43.3	112	8	ADR04194	E. cecorum
308	48	49.5	807	8	ADH01162	Human PRO	381	42	43.3	395	8	ADP25435	Plasmodiu
309	48	49.5	807	8	ADG69769	Novel hum	382	42	43.3	513	3	AAG11088	Arabidops
310	48	49.5	807	8	ADH02255	Human PRO	383	42	43.3	553	3	AAG11087	Arabidops
311	48	49.5	807	8	ADG69259	Novel hum	384	42	43.3	561	2	AAV41665	Zea mays
312	48	49.5	807	8	ADH86044	Novel hum	385	42	43.3	561	8	ADL18001	Maize OB-
313	48	49.5	807	8	ADH24980	Novel hum	386	42	43.3	574	3	AAG11086	Arabidops
314	48	49.5	807	8	ADH39597	Novel hum	387	42	43.3	716	3	AAG40451	Arabidops
315	48	49.5	807	8	ADH02595	Human PRO	388	42	43.3	747	3	AAG40450	Arabidops
316	48	49.5	807	8	ADG69089	Novel hum	389	42	43.3	815	8	ABM83993	Human dia

390	42	43.3	828	3	AAG40449	Ag40449 Arabidops	463	41	42.3	1286	3	AAG39101	Aag39101 Arabidops
391	42	43.3	840	4	AAM23903	Am23903 Human EST	464	40.5	41.8	1133	4	AAE04836	Aae04836 Human SGP
392	42	43.3	840	4	ABG01693	Abg01693 Novel hum	465	40.5	41.8	1196	5	ABP69057	Abp69057 Human pol
393	42	43.3	840	6	ABP54453	Abp54453 Desmocoll	466	40.5	41.8	1232	7	ADF53658	Adf53658 Human pol
394	42	43.3	878	2	AAR55060	Aar55060 Sequence	467	40	41.2	59	5	ABP00323	Abp00323 Human ORF
395	42	43.3	878	2	AAR55060	Aar55060 Sequence	468	40	41.2	95	5	ABM94641	Abm94641 M. xanthu
396	42	43.3	878	5	ABB81475	Abb81475 Human E-C	469	40	41.2	110	8	ADX87456	Adx87456 Plant ful
397	42	43.3	878	5	ADJ19323	Adj19323 Human E-C	470	40	41.2	158	8	ADX73384	Adx73384 Plant ful
398	42	43.3	882	2	AAV09375	Aav09375 Wild-type	471	40	41.2	195	6	ABU17509	Abu17509 Protein e
399	42	43.3	882	3	AAB35730	Aab35730 Human E-C	472	40	41.2	229	9	ADX07448	Adx07448 Cyclin-de
400	42	43.3	882	4	AAB73490	Aab73490 Human E-C	473	40	41.2	271	5	ABBS4619	Abbs4619 Lactococ
401	42	43.3	882	5	ABG96293	Abg96293 Human ova	474	40	41.2	352	8	ADR86042	Adr86042 Aspergill
402	42	43.3	882	5	AAU78051	Aau78051 Human E-C	475	40	41.2	367	6	ABU39548	Abu39548 Protein e
403	42	43.3	882	8	ADL15660	Adl15660 Human E-C	476	40	41.2	425	4	ABG02751	Abg02751 Novel hum
404	42	43.3	882	8	ADN03700	Adn03700 Antipori	477	40	41.2	510	4	ABM67810	Abm67810 Drosophil
405	42	43.3	882	8	ADP26906	Adp26906 Human E-C	478	40	41.2	600	6	ABM68570	Abm68570 Phototrab
406	42	43.3	882	8	ABM81765	Abm81765 Tumour-as	479	40	41.2	600	7	ADF03911	Adf03911 Bacterial
407	42	43.3	882	8	ADR67260	Adr67260 Human bla	480	40	41.2	604	7	ADD27964	Add27964 Mink COX
408	42	43.3	882	9	ABE87740	Abe87740 Human E-C	481	40	41.2	720	8	ADX67767	Adx67767 Plant ful
409	42	43.3	884	6	ABP54452	Abp54452 Desmocoll	482	40	41.2	753	5	ABB92299	Abb92299 Herbicida
410	42	43.3	894	8	ADX68263	Adx68263 Plant ful	483	40	41.2	753	8	ADT55831	Adt55831 Plant pol
411	42	43.3	896	8	ADR66291	Adr66291 Human pro	484	40	41.2	830	4	AAU09959	Aau09959 Human cad
412	42	43.3	896	8	ADR66852	Adr66852 Human pro	485	40	41.2	1042	8	ADQ97950	Adq97950 Human can
413	42	43.3	923	8	ADR66668	Adr66668 Human pro	486	40	41.2	1043	8	ADQ67640	Adq67640 Novel hum
414	42	43.3	923	8	ADR66326	Adr66326 Human pro	487	40	41.2	5147	4	ABBS9831	Abbs9831 Drosophil
415	42	43.3	1294	8	ADN24016	Adn24016 Bacterial	488	39.5	40.7	118	3	AAQ01741	Aaq01741 Human sec
416	42	43.3	1294	8	ADN24014	Adn24014 Bacterial	489	39.5	40.7	149	3	AAQ01740	Aaq01740 Human sec
417	42	43.3	4970	9	ABE00354	Abe00354 Placid t	490	39.5	40.7	176	4	AAAB90801	Aaab90801 Human she
418	41.5	42.8	281	4	ABBS2438	Abbs2438 Mycobacte	491	39.5	40.7	178	4	AAU28199	Aau28199 Novel hum
419	41	42.3	65	6	ABO04922	Abo04922 Human col	492	39.5	40.7	178	5	AAE22092	Aae22092 Human cav
420	41	42.3	74	9	ABE94348	Abe94348 Human AMD	493	39.5	40.7	178	5	AAU79340	Aau79340 Human cav
421	41	42.3	78	8	ADV89192	Adv89192 Streptoco	494	39.5	40.7	178	6	ABP96309	Abp96309 Human cav
422	41	42.3	78	8	ADV80445	Adv80445 Streptoco	495	39.5	40.7	178	7	ADB45024	Add45024 Rat Prote
423	41	42.3	92	4	AAI16599	Aai16599 Peptide #	496	39.5	40.7	178	7	ADI63101	Adi63101 Human apo
424	41	42.3	92	4	ABB35582	Abb35582 Peptide #	497	39.5	40.7	178	8	ADK70553	Adk70553 Respiro
425	41	42.3	92	4	AAI29083	Aai29083 Peptide #	498	39.5	40.7	178	8	ADL61216	Adl61216 Human pro
426	41	42.3	92	4	ABB30410	Abb30410 Peptide #	499	39.5	40.7	178	8	ADL61216	Adl61216 Human pro
427	41	42.3	92	4	ABB21009	Abb21009 Protein #	500	39.5	40.7	178	8	ABM80928	Abm80928 Tumour-as
428	41	42.3	92	4	AAI68777	Aai68777 Human bon							
429	41	42.3	92	4	AAI56397	Aai56397 Human bra							
430	41	42.3	92	4	ABG50442	Abg50442 Human liv							
431	41	42.3	92	4	AAI04312	Aai04312 Peptide #							
432	41	42.3	92	5	ABG38360	Abg38360 Human pep							
433	41	42.3	110	4	ABG26377	Abg26377 Novel hum							
434	41	42.3	170	2	AAI60535	Aai60535 Fragment							
435	41	42.3	208	5	ABP40223	Abp40223 Staphyloc							
436	41	42.3	208	8	ADS06613	Ads06613 Staphyloc							
437	41	42.3	301	4	AAI82366	Aai82366 S. epider							
438	41	42.3	302	8	ADX88450	Adx88450 Plant ful							
439	41	42.3	534	4	ABG01344	Abg01344 Novel hum							
440	41	42.3	626	2	AAI44008	Aai44008 Rabbit ei							
441	41	42.3	626	2	AAI49849	Aai49849 Haem-regu							
442	41	42.3	626	6	AAU97074	Aau97074 Rabbit ha							
443	41	42.3	626	6	ABU63415	Abu63415 Rabbit ha							
444	41	42.3	626	8	ADF78953	Adf78953 Rabbit ha							
445	41	42.3	626	9	ABE35102	Abe35102 Rabbit he							
446	41	42.3	629	5	ABB05679	Abb05679 Human nuc							
447	41	42.3	629	6	ABR41067	Abr41067 Human MAP							
448	41	42.3	629	6	ABU63412	Abu63412 Human hae							
449	41	42.3	629	8	ADF78950	Adf78950 Human hae							
450	41	42.3	629	9	ABE35099	Abe35099 Human hem							
451	41	42.3	630	4	AAI93882	Aai93882 Human pol							
452	41	42.3	630	4	ABM65664	Abm65664 Novel pro							
453	41	42.3	630	5	AAI47923	Aai47923 Human hei							
454	41	42.3	630	6	ABR41066	Abr41066 Human MAP							
455	41	42.3	630	8	ADI29272	Adi29272 Human MAR							
456	41	42.3	630	8	ADL31972	Adl31972 Human pro							
457	41	42.3	630	8	ADQ26065	Adq26065 Heme-regu							
458	41	42.3	630	8	ABM60844	Abm60844 Tumour-as							
459	41	42.3	634	4	AAI78404	Aai78404 Human pro							
460	41	42.3	656	4	AAI79388	Aai79388 Human pro							
461	41	42.3	1205	3	AAG39103	Aag39103 Arabidops							
462	41	42.3	1243	3	AAG39102	Aag39102 Arabidops							

ALIGNMENTS

RESULT 1

AAW07908
ID AAW07908 standard; protein; 614 AA.XX
AC AAW07908;XX
DT 29-JAN-1997 (first entry)XX
DE Pemphigus vulgaris antigen protein extracellular region.XX
KW Autoantibody; immunoglobulin G; IgG1; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
dermatology.XX
OS Homo sapiens.XX
PN JP08188540-A.XX
PD 23-JUL-1996.XX
PF 30-JUN-1995; 95JP-00165632.XX
PR 30-JUN-1994; 94JP-00173291.XX
PA (NISH/) NISHIKAWA T.XX
DR WPI; 1996-388562/39.XX
PT Fused protein recognised by Pemphigus vulgaris autoantibody - useful to
treat and diagnose P. vulgaris related diseases.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:09:24 ; Search time 39 Seconds
(without alignments)
46.875 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	999	1 IJHUG3	desmoglein 3 precu
2	81	83.5	1043	1 IJBOG1	desmoglein 1 precu
3	81	83.5	1049	1 IJHUG1	desmoglein 1 precu
4	71	73.2	1117	2 S57904	virR49 protein - hum
5	52	53.6	533	2 S57903	positive regulator
6	52	53.6	533	2 JCS040	cadherin 2 precurs
7	52	53.6	906	1 IJHUCN	N-cadherin precurs
8	49	50.5	877	1 IJBOCN	N-cadherin precurs
9	49	50.5	906	1 IJMSCN	N-cadherin precurs
10	48	49.5	829	2 I46536	Kep-cadherin - rab
11	47	48.5	317	2 B96963	uncharacterized co
12	46	47.4	783	2 I50116	N-cadherin precurs
13	45	46.4	620	2 A53731	translation initia
14	45	46.4	884	1 IJMSCE	B-cadherin precurs
15	45	46.4	884	2 S34438	uvomorulin - mouse
16	45	46.4	1321	2 T23476	hypothetical prote
17	45	46.4	1321	2 S27337	multidrug resistan
18	44	45.4	347	2 D69373	immunogenic protei
19	44	45.4	512	2 T38422	probable chromatin
20	44	45.4	905	1 IJXLC1	N-cadherin 1 precu
21	44	45.4	906	1 IJXLC2	N-cadherin 2 precu
22	44	45.4	1114	2 T25083	hypothetical prote
23	44	45.4	1158	2 T25082	hypothetical prote
24	43	44.3	307	2 T40240	dimethylase - fiss
25	43	44.3	315	2 T43249	rRNA (adenine-N6,N
26	43	44.3	480	2 T18675	hypothetical prote
27	43	44.3	725	1 E64211	virulence-associat
28	43	44.3	809	1 IJBODD	desmocollin 2b pre
29	43	44.3	827	2 A53954	LI-cadherin precu

30	43	44.3	863	1 IJBODC	desmocollin 2a pre
31	43	44.3	912	1 IJCHCN	N-cadherin precurs
32	42	43.3	388	2 T09489	hypothetical prote
33	42	43.3	479	2 T30794	hypothetical prote
34	42	43.3	479	2 T28480	hypothetical prote
35	42	43.3	479	2 H72155	CIL protein - vari
36	42	43.3	479	2 E42508	EIL protein - vacc
37	42	43.3	479	2 D36841	EIL protein - vari
38	42	43.3	487	2 F84751	hypothetical prote
39	42	43.3	533	2 E86412	hypothetical prote
40	42	43.3	761	1 IJBODE	desmocollin la - b
41	42	43.3	770	2 B48910	desmocollin lb pre
42	42	43.3	824	2 A48910	desmocollin la pre
43	42	43.3	839	1 IJBODF	desmocollin lb pre
44	42	43.3	840	2 I37281	Desla precursor -
45	42	43.3	873	2 F86426	95.1k hypothetical
46	42	43.3	882	1 IJHUCE	cadherin 1 precurs
47	42	43.3	894	2 I37282	Desclb precursor -
48	42	43.3	1294	2 T19982	hypothetical prote
49	41.5	42.8	281	2 D70845	hypothetical prote
50	41	42.3	355	2 T15203	hypothetical prote
51	41	42.3	598	2 AG0311	NADH2 dehydrogenas
52	41	42.3	626	2 A41284	translation initia
53	41	42.3	673	2 G85095	hypothetical prote
54	41	42.3	693	2 T47474	hypothetical prote
55	41	42.3	732	1 IJCHCB	B-cadherin precurs
56	41	42.3	1286	2 A42150	P-glycoprotein pgp
57	40.5	41.8	399	2 T33059	hypothetical prote
58	40	41.2	102	2 S45807	probable membrane
59	40	41.2	139	2 AH3595	fosfomycin resista
60	40	41.2	163	2 AF2504	hypothetical prote
61	40	41.2	208	2 T24446	hypothetical prote
62	40	41.2	228	2 C26599	clathrin light cha
63	40	41.2	229	2 B31775	clathrin light cha
64	40	41.2	231	2 T21119	hypothetical prote
65	40	41.2	236	2 D71733	phosphoribosylamin
66	40	41.2	238	1 LRRTB2	clathrin light cha
67	40	41.2	271	2 B86785	glutamate racemase
68	40	41.2	327	2 T19782	hypothetical prote
69	40	41.2	731	2 C84464	Mutator-like trans
70	40	41.2	735	2 T12986	hypothetical prote
71	40	41.2	914	2 T08952	hypothetical prote
72	40	41.2	960	2 D85095	hypothetical prote
73	40	41.2	1421	2 T02501	hypothetical prote
74	40	41.2	5147	1 IJFETM	cadherin-related t
75	39.5	40.7	178	2 S25884	caveolin - human
76	39.5	40.7	178	2 A43419	vesicular integral
77	39.5	40.7	178	2 I48976	caveolin alpha for
78	39.5	40.7	200	2 A46424	caveolin - chicken
79	39.5	40.7	432	2 T33118	hypothetical prote
80	39.5	40.7	514	2 D86280	protein T5E21.7 [i
81	39	40.2	89	2 C89447	protein F57C12.1 [i
82	39	40.2	231	2 E97280	amidase, germinati
83	39	40.2	236	2 F97736	hypothetical prote
84	39	40.2	288	2 B84862	hypothetical prote
85	39	40.2	320	2 S73186	cytochrome f - red
86	39	40.2	335	2 AF1565	teichoic acid tran
87	39	40.2	353	2 AB3296	hypothetical prote
88	39	40.2	381	2 H83985	alpha-D-mannose-al
89	39	40.2	461	2 D64701	thiophene and fura
90	39	40.2	461	2 G71818	probable thiophene
91	39	40.2	577	2 H82544	pilus biogenesis p
92	39	40.2	584	2 S75944	hypothetical prote
93	39	40.2	588	2 E87521	peptidase M1 famil
94	39	40.2	726	1 S73915	virulence-associat
95	39	40.2	811	2 T48468	disease resistance
96	39	40.2	822	1 IJMSCP	P-cadherin precurs
97	39	40.2	879	2 T50388	hypothetical prote
98	39	40.2	1095	2 PC1114	SKCQ25 protein -
99	38.5	39.7	124	2 B89831	staphylococcal acc
100	38.5	39.7	375	2 A85890	N-succinyl-diamino
101	38.5	39.7	375	2 A42959	succinyl-diaminopi
102	38.5	39.7	375	2 F91045	N-succinyl-diamino

103	38.5	39.7	812	2	T52569	squamosa-promoter	176	37	38.1	304	2	DB2189	conserved hypotet
104	38.5	39.7	1035	2	G86342	hypothetical prote	177	37	38.1	305	2	H95171	glycyl-tRNA synthe
105	38	39.2	126	2	E84047	hypothetical prote	178	37	38.1	305	2	H98037	glycine-tRNA ligas
106	38	39.2	137	2	S55915	ribosomal protein	179	37	38.1	308	2	B70103	methylenetetrahydr
107	38	39.2	137	2	I48738	ribosomal protein	180	37	38.1	320	1	CFR2	plastoquinol-plast
108	38	39.2	138	2	S74520	hypothetical prote	181	37	38.1	320	2	S07296	plastoquinol-plast
109	38	39.2	189	2	T47133	hypothetical prote	182	37	38.1	320	2	S58564	plastoquinol-plast
110	38	39.2	221	1	S71905	probable nonhiston	183	37	38.1	320	2	A26576	sfmH protein limpo
111	38	39.2	237	2	JQ0729	60K inner-membrane	184	37	38.1	325	2	C90703	protein involved i
112	38	39.2	265	2	A26771	CCAAR-binding fact	185	37	38.1	325	2	F85553	sfmH protein precu
113	38	39.2	279	2	T33429	hypothetical prote	186	37	38.1	325	2	D64785	hypothetical prote
114	38	39.2	296	2	D98345	SN-glycerol-3-phos	187	37	38.1	330	2	T22411	plastoquinol-plast
115	38	39.2	296	2	AC2937	hypothetical prote	188	37	38.1	342	1	CPBM	protein T2787.7 [i
116	38	39.2	311	2	AF0150	probable outer mem	189	37	38.1	357	2	A88969	probable endonucle
117	38	39.2	313	2	C84724	hypothetical prote	190	37	38.1	361	2	F71560	probable transketol
118	38	39.2	317	2	G86761	hypothetical prote	191	37	38.1	367	2	B72644	hypothetical prote
119	38	39.2	318	2	S00431	plastoquinol-plast	192	37	38.1	381	2	T38655	hypothetical 37.5
120	38	39.2	320	1	CFNT	plastoquinol-plast	193	37	38.1	396	2	B81299	probable molybdopt
121	38	39.2	333	2	S49752	dipeptide transpor	194	37	38.1	397	2	E97176	N-terminal domain
122	38	39.2	335	2	H98352	FimH protein precu	195	37	38.1	403	2	B64583	conserved hypotet
123	38	39.2	342	2	AF2929	hypothetical prote	196	37	38.1	406	2	E71928	probable outer mem
124	38	39.2	368	1	H64063	gcPE protein - Hae	197	37	38.1	448	2	E96837	unknown protein T2
125	38	39.2	376	2	B72321	conserved hypotet	198	37	38.1	461	2	A71662	sodium/pantothemat
126	38	39.2	385	2	S48752	homeotic protein Y	199	37	38.1	490	1	VCCV3	coat protein - cau
127	38	39.2	392	2	S34823	dehydratase-induce	200	37	38.1	493	1	S39532	aldehyde dehydroge
128	38	39.2	418	2	E86171	hypothetical prote	201	37	38.1	501	2	S23374	uridine kinase (EC
129	38	39.2	429	2	JC4656	rRNA endonuclease	202	37	38.1	505	2	T19106	probable serine ca
130	38	39.2	456	2	T48478	serine/threonine p	203	37	38.1	505	2	S63994	protein disulfide-
131	38	39.2	461	2	B88953	protein F1684.8 [i	204	37	38.1	580	1	EKECEX	gamma-glutamyltran
132	38	39.2	461	2	T32663	hypothetical prote	205	37	38.1	580	2	ABO994	gamma-glutamyltran
133	38	39.2	463	2	H87280	adenosylhomocystei	206	37	38.1	581	2	E91165	gamma-glutamyltran
134	38	39.2	538	2	A31760	Ro/SS-A complex, 6	207	37	38.1	581	2	E86011	gamma-glutamyltran
135	38	39.2	553	2	AF1113	hypothetical prote	208	37	38.1	593	2	D83316	NADH dehydrogenase
136	38	39.2	560	2	T71621	exonuclease domain	209	37	38.1	600	2	AD0797	NADH2 dehydrogenas
137	38	39.2	566	2	T47934	hypothetical prote	210	37	38.1	619	1	KGBOH2	kininogen, HMW II
138	38	39.2	578	2	T02292	hypothetical prote	211	37	38.1	621	1	KGBOH1	kininogen, HMW I p
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143	38	39.2	640	2	B90590	hypothetical prote	216	37	38.1	644	2	H85788	hypothetical prote
144	38	39.2	655	2	H82938	probable ABC subst	217	37	38.1	651	2	G71697	probable soluble l
145	38	39.2	716	2	T01802	hypothetical prote	218	37	38.1	653	2	T40185	n-acetylglucosamin
146	38	39.2	721	2	C82939	virulence associat	219	37	38.1	686	2	T25987	hypothetical prote
147	38	39.2	832	2	S55396	Li-cadherin - huma	220	37	38.1	689	1	S25621	UDPglucose 4-epime
148	38	39.2	834	2	T29821	hypothetical prote	221	37	38.1	695	2	T40717	hypothetical prote
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150	38	39.2	901	1	IJHUDA	desmocollin 3a pre	223	37	38.1	759	2	AF1449	hypothetical prote
151	38	39.2	905	2	S43064	cadherin - African	224	37	38.1	800	2	S54623	desmocollin, type
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154	38	39.2	1231	2	AF2220	hypothetical prote	227	37	38.1	876	2	G90592	hypothetical prote
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156	38	39.2	1583	2	T00727	myosin heavy chain	229	37	38.1	896	2	I45858	desmocollin - bovi
157	38	39.2	2278	1	S56274	FAB1 protein - yea	230	37	38.1	958	1	P1BVCC	1a protein - cowpe
158	37.5	38.7	440	2	S42953	hypothetical prote	231	37	38.1	1113	2	T45822	hypothetical prote
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160	37.5	38.7	586	2	F64186	ABC-type transport	233	37	38.1	1556	2	F96587	hypothetical prote
161	37.5	38.7	647	2	T52568	squamosa-promoter	234	37	38.1	1798	2	T27149	hypothetical prote
162	37.5	38.7	775	2	T07172	subtilisin-like pr	235	37	38.1	1815	2	F73021	polyketide synthas
163	37.5	38.7	1020	2	H96793	unknown protein p1	236	37	38.1	1822	2	S87203	polyketide synthas
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173	37	38.1	283	2	D72398	conserved hypotet	246	36	37.1	109	2	B82210	sulfite reductase,
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175	37	38.1	302	2	AF1654	L-lactate dehydrog	248	36	37.1	115	2	B84969	flagellar basal-bo

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DNA polymerase III
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GMP synthase [glut
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ALIGNMENTS

RESULT 1

IJHUG3

desmoglein 3 precursor - human

N;Alternate names: pemphigus vulgaris antigen

C;Species: Homo sapiens (nan)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: A41088

R;Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R.

Cell 67, 869-877, 1991

A;Title: Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a dis

A;Reference number: A41088; MUID:92069753; PMID:1720352

A;Accession: A41088

A;Molecule type: mRNA

A;Residues: 1-999 <AMA>

A;Cross-references: UNIPROT:P32926; UNIPARC:UPI000004CAAC; GB:M76482; NID:9190751; PIDN:

C;Genetics:

A;Gene: GDB:DSG3

A;Cross-references: GDB:134030; OMIM:169615

A;Map position: 18q12.1-18q12.2

C;Superfamily: cadherin; cadherin repeat homolog

C;Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-49/Domain: propeptide #status predicted <PRO>

F;50-999/Product: desmoglein homolog #status predicted <MAT>

F;50-615/Domain: extracellular #status predicted <EXT>

F;52-157/Domain: cadherin repeat homolog <CR1>

F;160-267/Domain: cadherin repeat homolog <CR2>

F;270-383/Domain: cadherin repeat homolog <CR3>

F;390-495/Domain: cadherin repeat homolog <CR4>

F;496-598/Domain: cadherin repeat homolog <CR5>

F;616-639/Domain: transmembrane #status predicted <TM>

F;640-999/Domain: intracellular #status predicted <INT>

F;910-938/Domain: desmoglein repeat <DG1>

F;937-966/Domain: desmoglein repeat <DG2>

F;110,180,545/Binding site: carbohydrate (Asn) (covalent) #status predicted

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:09:03 ; Search time 228 Seconds
(without alignments)
58.794 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	993	1	DSG3 CANFA
2	97	100.0	999	1	DSG3 HUMAN
3	95	97.9	993	1	DSG3 MOUSE
4	85	87.6	1040	1	DSG4 RAT
5	85	87.6	1041	1	DSG4 MOUSE
6	83	85.6	1040	1	DSG4 HUMAN
7	81	83.5	1043	1	DSG1 BOVIN
8	81	83.5	1049	1	DSG1 HUMAN
9	81	83.5	1054	1	DSG1 CANFA
10	75	77.3	911	1	DSG1C MOUSE
11	75	77.3	1057	1	DSG1A MOUSE
12	75	77.3	1060	1	DSG1B MOUSE
13	71	73.2	1117	1	DSG2 HUMAN
14	71	73.2	1118	2	Q4KKU6 HUMAN
15	65	67.0	292	2	Q8VCE3 MOUSE
16	65	67.0	360	2	Q81111 MOUSE
17	65	67.0	1122	1	DSG2 MOUSE
18	62	63.9	776	2	Q4T7X7 TETNG
19	59	60.8	310	2	Q4T7X8 TETNG
20	59	60.8	680	2	Q4S260 TETNG
21	59	60.8	1101	2	Q4T7X6 TETNG
22	54	55.7	344	2	Q4TGV6 TETNG
23	54	55.7	639	2	Q7Y0F5 ORISA
24	54	55.7	728	2	Q4SDX7 TETNG
25	54	55.7	864	2	Q7XVY5 ORISA
26	53	54.6	200	2	Q8SD26 9CAUD
27	52	53.6	530	2	Q4QSR3 STRPY
28	52	53.6	533	2	Q54989 STRPY
29	52	53.6	533	2	Q54891 STRPY
30	52	53.6	533	2	Q4QSR0 STRPY
31	52	53.6	533	2	Q4QSR6 STRPY

32	52	53.6	533	2	Q4QSR7 STRPY	Q4QSR7 streptococc
33	52	53.6	533	2	Q4QSR8 STRPY	Q4QSR8 streptococc
34	52	53.6	533	2	Q4QSR9 STRPY	Q4QSR9 streptococc
35	52	53.6	533	2	Q8NZ78 STRP8	Q8NZ78 streptococc
36	52	53.6	906	1	CADH2 HUMAN	P19022 homo sapien
37	52	53.6	906	2	Q8N173 HUMAN	Q8N173 homo sapien
38	51	52.6	533	2	Q4QSR1 STRPY	Q4QSR1 streptococc
39	51	52.6	533	2	Q4QSR4 STRPY	Q4QSR4 streptococc
40	51	52.6	533	2	Q4QSR5 STRPY	Q4QSR5 streptococc
41	50	51.5	742	2	Q6GL53_XENTR	Q6GL53 xenopus tro
42	49	50.5	238	1	CADH2_CRIGR	Q55075 cricetus
43	49	50.5	707	2	Q8S5J8_RHILO	Q8S5J8 rhizobium l
44	49	50.5	875	2	Q5RB18_PONPY	Q5RB18 pongo pygma
45	49	50.5	877	1	CADH2_BOVIN	P15534 bos taurus
46	49	50.5	906	1	CADH2_MOUSE	P15116 mus musculu
47	49	50.5	906	1	CADH2_RAT	Q321V3 rattus norv
48	49	50.5	906	2	Q5R9X1_PONPY	Q5R9X1 pongo pygma
49	49	50.5	906	2	Q8BS19_MOUSE	Q8BS19 mus musculu
50	49	50.5	906	2	Q6GU11_MOUSE	Q6GU11 mus musculu
51	48	49.5	560	2	Q5CPQ5_CRYPV	Q5CPQ5 cryptospori
52	48	49.5	560	2	Q5CGA4_CRYHO	Q5CGA4 cryptospori
53	48	49.5	829	1	CAD16_HUMAN	Q75309 homo sapien
54	48	49.5	829	1	CAD16_RABIT	Q28634 oryctolagus
55	47.5	49.0	464	2	Q89QR0_BRAJA	Q89QR0 bradyrhizob
56	47	48.5	317	2	Q97LP1_CLOAB	Q97LP1 clostridium
57	47	48.5	749	2	Q5R5C7_PONPY	Q5R5C7 pongo pygma
58	47	48.5	903	2	Q5H299_XENIA	Q5H299 xenopus lae
59	46.5	47.9	517	2	Q52D84_MAGGR	Q52D84 magnaportha
60	46.5	47.9	595	2	Q4IED9_GIBZE	Q4IED9 gibberella
61	46	47.4	249	2	Q6DC16_BRARE	Q6DC16 brachydanio
62	46	47.4	299	1	HIS1_PASMU	P57919 pasteurella
63	46	47.4	307	2	Q5UQC4_MIMIV	Q5UQC4 mimivirus
64	46	47.4	334	2	Q9Z643_ENTCL	Q9Z643 enterobacte
65	46	47.4	471	2	Q4N505_THEPA	Q4N505 theileria p
66	46	47.4	548	2	Q5WJY6_BACSK	Q5WJY6 bacillus cl
67	46	47.4	734	2	Q4SJS0_TETNG	Q4SJS0 tetraodon n
68	46	47.4	827	1	CAD17_MOUSE	Q91100 mus musculu
69	46	47.4	893	1	CADH2_BRARE	Q90275 brachydanio
70	45	46.4	224	2	Q5CE69_CRYHO	Q5CE69 cryptospori
71	45	46.4	356	2	Q61CY6_CABBR	Q61CY6 caenorhabdi
72	45	46.4	459	1	DNAA_NITEU	Q82Y84 nitrosomona
73	45	46.4	619	1	E2AK1_MOUSE	Q92259 m eukaryoti
74	45	46.4	620	1	E2AK1_RAT	Q63185 r eukaryoti
75	45	46.4	620	2	Q642C7_RAT	Q642C7 rattus norv
76	45	46.4	635	2	Q69ZK8_MOUSE	Q69ZK8 mus musculu
77	45	46.4	829	2	Q5E9G7_BOVIN	Q5E9G7 bos taurus
78	45	46.4	884	1	CADH1_MOUSE	Q59803 mus musculu
79	45	46.4	884	2	Q4KML8_MOUSE	Q4KML8 mus musculu
80	45	46.4	1321	1	MDR1_CAEEL	P34712 caenorhabdi
81	44.5	45.9	375	2	Q7N3J4_PHOLL	Q7N3J4 photorhabdu
82	44	45.4	207	2	Q4RHU3_TETNG	Q4RHU3 tetraodon n
83	44	45.4	323	2	Q5SFP4_DICDI	Q5SFP4 dictyosteli
84	44	45.4	328	2	Q7RTS3_HUMAN	Q7RTS3 homo sapien
85	44	45.4	347	2	Q29274_ARCFU	Q29274 archaeoglob
86	44	45.4	441	2	Q97300_PLAF7	Q97300 plasmodium
87	44	45.4	484	1	MYPT2_MOUSE	Q8BG95 mus musculu
88	44	45.4	512	2	Q13985_SCHPO	Q13985 schizosacch
89	44	45.4	609	2	Q6BL55_DEBHA	Q6BL55 debaryomyce
90	44	45.4	887	1	SYA_BARHE	Q6G224 bartonella
91	44	45.4	905	1	CADHN_XENLA	P20310 xenopus lae
92	44	45.4	906	1	CADHO_XENLA	P33147 xenopus lae
93	44	45.4	1225	2	Q22656_CABEL	Q22656 caenorhabdi
94	44	45.4	1263	2	Q22655_CABEL	Q22655 caenorhabdi
95	44	45.4	1732	2	Q963J6_HELVI	Q963J6 heliothis v
96	43.5	44.8	1928	2	Q8T9H1_DROME	Q8T9H1 drosophila
97	43.5	44.8	2280	2	Q9V8E6_DROME	Q9V8E6 drosophila
98	43.5	44.8	2302	2	Q9N693_DROME	Q9N693 drosophila
99	43.5	44.8	2310	2	Q9GPA9_DROME	Q9GPA9 drosophila
100	43	44.3	66	2	Q7WXC8_ALECU	Q7WXC8 alcaligenes
101	43	44.3	99	2	Q9UAD7_HAECC	Q9UAD7 haemochus
102	43	44.3	99	2	Q9UAD8_HAECC	Q9UAD8 haemochus
103	43	44.3	100	2	Q9UAD4_HAECC	Q9UAD4 haemochus
104	43	44.3	100	2	Q9UAD5_HAECC	Q9UAD5 haemochus

105	43	44.3	100	2	Q9UAD6_HAECO	Q9uad6 haemochus	178	42	43.3	624	2	Q9CUC0_MOUSE	Q9cuc0 mus musculus
106	43	44.3	100	2	Q9UAD9_HAECO	Q9uad9 haemochus	179	42	43.3	693	2	Q4HWT6_GIBZE	Q4hwt6 gibberella
107	43	44.3	100	2	Q9UAE3_HAECO	Q9uad3 haemochus	180	42	43.3	697	2	Q7QDT2_ANOGA	Q7qdt2 anopheles g
108	43	44.3	145	1	CADH3_FIG	O18926 sus scrofa	181	42	43.3	714	2	Q5TNG3_ANOGA	Q5tng3 anopheles g
109	43	44.3	272	2	Q889A5_PSESM	Q889a5 pseudomonas	182	42	43.3	748	2	Q76EK8_MORBO	Q76ek8 moraxella b
110	43	44.3	307	1	DIM1_SCHPO	Q9usut2 schizosacch	183	42	43.3	821	2	Q9UII8_HUMAN	Q9uii8 homo sapien
111	43	44.3	325	2	Q55KJ5_CRYNE	O55kj5 cryptococcu	184	42	43.3	840	2	Q9HB00_HUMAN	Q9hb00 homo sapien
112	43	44.3	325	2	Q5KAX6_CRYNE	O5kax6 cryptococcu	185	42	43.3	873	2	Q9C756_ARATH	Q9c756 arabidopsis
113	43	44.3	333	2	Q4YW59_PLABE	Q4yw59 plasmodium	186	42	43.3	882	1	CADH1_HUMAN	P12830 homo sapien
114	43	44.3	355	2	Q54XG6_DICDI	Q54xg6 dictyosteli	187	42	43.3	882	2	Q5RAX1_PONPY	Q5rax1 pongo pygma
115	43	44.3	376	2	Q4SD35_TETNG	Q4sd35 tetraodon n	188	42	43.3	886	1	CADH1_RAT	Q9rtc4 rattus norv
116	43	44.3	480	2	Q9XVF8_CAEEL	Q9xvf8 caenorhabdi	189	42	43.3	893	1	DSC1_HUMAN	Q01107 bos taurus
117	43	44.3	515	2	Q4UHC4_THEAN	O4uhc4 theileria a	190	42	43.3	894	1	Q9HB01_HUMAN	Q9hb01 homo sapien
118	43	44.3	571	2	Q7YN58_EIMTE	Q7yn58 eimeria ten	191	42	43.3	894	2	Q9UII7_HUMAN	Q9uii7 homo sapien
119	43	44.3	578	2	Q63423_RAT	Q63423 rattus norv	192	42	43.3	901	2	Q9UII7_HUMAN	Q9uii7 homo sapien
120	43	44.3	725	1	RNR_MYCGE	P47350 mycoplasma	193	42	43.3	943	2	Q554N4_DICDI	Q554n4 dictyosteli
121	43	44.3	756	2	Q9FIS9_ARATH	Q9fis9 arabidopsis	194	42	43.3	959	2	Q80XQ5_MOUSE	Q80xq5 mus musculus
122	43	44.3	814	2	Q6FXZ2_CANGA	O6fxz2 candida gla	195	42	43.3	970	2	Q6A000_MOUSE	Q6a000 mus musculus
123	43	44.3	816	2	Q94BP0_ARATH	Q94bp0 arabidopsis	196	42	43.3	1143	2	Q6MAW0_PARUM	Q6maw0 parachlamyd
124	43	44.3	827	1	CAD17_RAT	P55281 rattus norv	197	42	43.3	1294	2	O45721_CABEL	O45721 caenorhabdi
125	43	44.3	863	1	DSC2_BOVIN	P33545 bos taurus	198	42	43.3	1294	2	Q61TP6_CABBR	Q61tp6 caenorhabdi
126	43	44.3	867	1	GLR12_ARATH	Q91v72 arabidopsis	199	42	43.3	1511	2	Q89715_CLOTE	Q89715 clostridium
127	43	44.3	868	2	Q6P3M3_BRARE	O6p3m3 brachydanio	200	42	43.3	2087	2	Q4Q3E0_LETMA	Q4q3e0 leishmania
128	43	44.3	868	2	Q90X63_BRARE	O90x63 brachydanio	201	41.5	42.8	45	2	Q5BYM7_SCHJA	Q5bym7 schistosoma
129	43	44.3	868	2	Q803S8_BRARE	O803s8 brachydanio	202	41.5	42.8	265	2	Q7D5P3_MYCTU	Q7dsp3 mycobacteri
130	43	44.3	912	1	CADH2_CHICK	P10288 gallus gall	203	41.5	42.8	281	2	O53383_MYCTU	O53383 mycobacteri
131	43	44.3	1099	2	O518U7_ENTHI	Q518u7 entamoeba h	204	41.5	42.8	281	2	Q7TWPS_MYCBO	Q7twps mycobacteri
132	43	44.3	1364	2	Q6SLE1_COCHE	O6sle1 coeliobolu	205	41	42.3	64	2	Q87S22_VIBPA	Q87s22 vibrio para
133	43	44.3	1413	2	Q4MM45_BACCE	O4mm45 bacillus ce	206	41	42.3	95	2	Q6EEV6_HUMAN	Q6eev6 homo sapien
134	43	44.3	1732	2	O5QD53_HELVI	O5qd53 heliothis v	207	41	42.3	230	2	Q4NKM8_9M1CC	Q4nkm8 arthrobaete
135	42.5	43.8	127	2	O54NG1_DICDI	O54ng1 dictyosteli	208	41	42.3	241	2	O4N319_THEPA	O4n319 theileria p
136	42.5	43.8	148	2	Q6YLH8_BRARE	O6ylh8 brachydanio	209	41	42.3	243	2	Q75MW7_HUMAN	Q75mw7 homo sapien
137	42.5	43.8	181	1	CAV1_FUGRU	Q9ygm8 fugu rubrip	210	41	42.3	268	2	Q812M6_PLAF7	Q812m6 plasmodium
138	42.5	43.8	181	2	Q6YLH9_BRARE	O6ylh9 brachydanio	211	41	42.3	271	2	Q4UAC9_THEAN	Q4uac9 theileria a
139	42.5	43.8	181	2	Q4RSH4_TETNG	O4rsh4 tetraodon n	212	41	42.3	271	2	Q5M115_STRT1	Q5m115 streptococ
140	42	43.3	207	2	Q6ZEU6_SYNY3	O6zeu6 synechocyst	213	41	42.3	271	2	Q5M627_STRT2	Q5m627 streptococ
141	42	43.3	219	2	O5WTF7_LEGPL	O5wtf7 legionella	214	41	42.3	277	2	Q7MRU2_WOISU	Q7mru2 wolinnella s
142	42	43.3	219	2	Q5Z876_LEGPH	O5z876 legionella	215	41	42.3	282	2	O8BNQ1_MOUSE	O8bnq1 mus musculus
143	42	43.3	260	2	Q850Z3_ORISA	Q850z3 oryza sativ	216	41	42.3	301	2	Q5NNH5_STAEP	Q5nnh5 staphylococ
144	42	43.3	309	2	Q8C913_MOUSE	Q8c913 mus musculus	217	41	42.3	301	2	Q8CNW0_STAEP	Q8cnw0 staphylococ
145	42	43.3	317	2	O54US9_DICDI	O54u9 dictyosteli	218	41	42.3	310	2	Q7VDC1_PROMA	Q7vdc1 prochloroco
146	42	43.3	347	2	Q9SHR1_ARATH	O9shr1 arabidopsis	219	41	42.3	321	2	Q7TR29_MOUSE	Q7tr29 mus musculus
147	42	43.3	376	2	O5V880_HALMA	O5v880 haloarcula	220	41	42.3	321	2	O8VGA7_MOUSE	O8vga7 mus musculus
148	42	43.3	388	2	Q48379_BPPL	Q48379 bacterioph	221	41	42.3	348	2	Q9T9L0_SATJU	Q9t9l0 satanoperc
149	42	43.3	392	2	Q8RWL7_ARATH	Q8rw17 arabidopsis	222	41	42.3	351	2	Q6C2D8_YARLI	Q6c2d8 yarrowia li
150	42	43.3	406	2	Q8IM17_PLAF7	Q8im17 plasmodium	223	41	42.3	355	2	O01810_CAEEL	O01810 caenorhabdi
151	42	43.3	417	2	Q86KC4_DICDI	Q86kc4 dictyosteli	224	41	42.3	357	2	Q4X799_PLACH	Q4x799 plasmodium
152	42	43.3	421	2	O54HY8_DICDI	O54hy8 dictyosteli	225	41	42.3	426	2	Q6BWE8_DEBHA	Q6bwe8 debaryomyce
153	42	43.3	477	2	Q71TD2_BPPL	Q71td2 bacterioph	226	41	42.3	468	2	Q7PIG4_CHRVO	Q7pig4 chromobacte
154	42	43.3	479	1	PAP1_VACCA	O57184 vaccinia vi	227	41	42.3	484	2	O541Z8_DICDI	O541z8 dictyosteli
155	42	43.3	479	1	PAP1_VACCC	P21079 vaccinia vi	228	41	42.3	507	2	Q8R0K2_MOUSE	Q8r0k2 mus musculus
156	42	43.3	479	1	PAP1_VACCV	P23371 vaccinia vi	229	41	42.3	544	2	Q89QL7_BRAJA	Q89ql7 brachyhib
157	42	43.3	479	1	PAP1_VARV	P33809 variola vir	230	41	42.3	548	2	Q4X1P1_ASPPU	Q4x1p1 aspergillus
158	42	43.3	479	2	O51XK5_MONPV	O5ixk5 monkeypox v	231	41	42.3	557	2	Q4S286_TETNG	Q4s286 tetraodon n
159	42	43.3	479	2	O6RZP5_9POXV	O6rzp5 rabbitpox v	232	41	42.3	592	2	Q4PB22_USMA	Q4pb22 ustilago ma
160	42	43.3	479	2	Q76Q36_VARV	Q76q36 variola min	233	41	42.3	595	2	Q8IDG1_PLAF7	Q8idg1 plasmodium
161	42	43.3	479	2	Q8QMZ9_COWPX	Q8qms9 cowpox viru	234	41	42.3	598	2	Q8ZDK9_YERPE	Q8zdk9 yersinia pe
162	42	43.3	479	2	Q8Q6Q7_CAMPS	Q8q67 camelpox vi	235	41	42.3	598	2	Q669A2_YERPS	Q669a2 yersinia ps
163	42	43.3	479	2	Q8V2M4_CAMPM	Q8v2m4 camelpox v	236	41	42.3	626	1	E2AK1_RABIT	P33279 o eukaryoti
164	42	43.3	479	2	Q8V530_MONPV	Q8v530 monkeypox v	237	41	42.3	630	1	E2AK1_HUMAN	Q9bq13 h eukaryoti
165	42	43.3	479	2	Q9JPD9_VACCT	O9jfd9 vaccinia v	238	41	42.3	630	2	O549K6_HUMAN	O549k6 homo sapien
166	42	43.3	479	2	Q9PX81_VARV	Q9px81 variola vir	239	41	42.3	631	2	Q4R8E0_MACFA	Q4r8e0 macaca fasc
167	42	43.3	479	2	Q80E12_COWPX	Q80e12 cowpox viru	240	41	42.3	657	2	Q6CXS0_KLULA	Q6cxso kluyveromyc
168	42	43.3	479	2	Q85370_VARV	Q85370 variola maj	241	41	42.3	660	2	Q4IR85_GIBZE	Q4ir85 gibberella
169	42	43.3	479	2	Q8JLG4_9POXV	O8jlg4 ectromelia	242	41	42.3	673	2	Q7FIJ2_ARATH	Q7fij2 arabidopsis
170	42	43.3	489	2	O81DC9_BACCK	Q81dc9 bacillus ce	243	41	42.3	693	2	Q9M3E4_ARATH	Q9m3e4 arabidopsis
171	42	43.3	515	2	O51WB6_MAGGR	O51wb6 magnaporthe	244	41	42.3	719	2	Q8CB32_MOUSE	Q8cb32 mus musculus
172	42	43.3	533	2	Q9LP33_ARATH	Q9lp33 arabidopsis	245	41	42.3	732	1	CADHK_CHICK	P33145 gallus gall
173	42	43.3	537	2	Q6Z6S1_ORISA	Q6z6s1 oryza sativ	246	41	42.3	734	2	Q6AC89_LEIXX	Q6ac89 leifsonia x
174	42	43.3	537	2	Q846P6_9CYAN	Q846p6 lyngbya maj	247	41	42.3	781	2	Q7M7N9_WOISU	Q7m7n9 wolinnella s
175	42	43.3	553	2	O22957_ARATH	O22957 arabidopsis	248	41	42.3	814	2	Q77704_CANFA	Q77704 canis famil
176	42	43.3	556	2	Q8GXH2_ARATH	Q8gxh2 arabidopsis	249	41	42.3	832	2	Q8C4K6_MOUSE	Q8c4k6 mus musculus
177	42	43.3	574	2	Q4S5J7_TETNG	Q4s5j7 tetraodon n	250	41	42.3	856	1	K1115_MOUSE	Q7tsi3 mus musculus

251	41	42.3	886	1	DSC1_MOUSE	P55849	mus musculus	324	40	41.2	480	2	Q556A8_DICD1	Q556A8 dictyosteli
252	41	42.3	920	2	Q4SDX5_TETNG	Q4sdx5 tetraodon n	325	40	41.2	482	1	HLDE_HELHP	Q7Vf23 helicobacte	
253	41	42.3	976	2	Q601C3_MYCHY	Q601c3 mycoplasma	326	40	41.2	498	2	Q710D7_VULVU	Q710d7 vulpes vulp	
254	41	42.3	977	2	Q841I7_GLONO	Q841i7 glostridium	327	40	41.2	510	2	Q9VL73_DROME	Q9v173 drosophila	
255	41	42.3	1079	2	Q41DT9_GIBZE	Q41dt9 gibberella	328	40	41.2	512	2	Q6R7M3_DIPPU	Q6r7m3 diploptera	
256	41	42.3	1286	2	Q8L6X6_ARATH	Q8L6x6 arabidopsis	329	40	41.2	546	2	Q7T2S1_FUGRU	Q7t2s1 fugu rubrip	
257	41	42.3	1286	2	Q9ZR72_ARATH	Q9zr72 arabidopsis	330	40	41.2	559	2	Q69M85_ORYSA	Q69m85 oryza sativ	
258	41	42.3	2202	2	Q6BPU1_DEBHA	Q6bpu1 debaryomyce	331	40	41.2	567	2	Q4S315_TETNG	Q4s315 tetraodon n	
259	41	42.3	2241	2	Q91HJ2_9PARA	Q91hj2 avian param	332	40	41.2	568	2	Q5RH90_BRARE	Q5rh90 brachydanio	
260	41	42.3	2422	2	Q9NKN9_LEIMA	Q9nkn9 leishmania	333	40	41.2	598	2	Q7N219_PHOEL	Q7n219 photorhabdo	
261	40.5	41.8	387	2	Q4FKY7_9RICK	Q4fky7 candidatus	334	40	41.2	599	2	Q6D2R9_ERWCT	Q6d2r9 erwinia car	
262	40.5	41.8	395	2	Q9PTY3_LAMRE	Q9ptx5 lampetra re	335	40	41.2	604	1	PGH2_MUSVI	Q62725 mustela vis	
263	40.5	41.8	399	2	Q617S6_CAEEL	Q617s6 caenorhabdi	336	40	41.2	612	2	Q812V3_PLAF7	Q812v3 plasmodium	
264	40.5	41.8	562	2	Q51BF7_ENTHI	Q51bf7 entamoeba h	337	40	41.2	631	2	Q55MB7_CRYNE	Q55mb7 cryptococcu	
265	40.5	41.8	649	2	Q52BM2_MAGGR	Q52bm2 magnapoorth	338	40	41.2	631	2	Q5K8F6_CRYNE	Q5k8f6 cryptococcu	
266	40.5	41.8	1158	2	Q5V2P5_HUMAN	Q5vzps homo sapien	339	40	41.2	655	2	Q96TW7_HANAN	Q96tw7 hansanula a	
267	40	41.2	64	2	Q8DEZ3_VIBVU	Q8dez3 vibrio vuln	340	40	41.2	679	2	Q5CHM4_CRYHO	Q5chm4 cryptospori	
268	40	41.2	67	2	Q6FCU2_ACIAD	Q6fcu2 acinetobact	341	40	41.2	682	2	Q5A2J6_CANAL	Q5a2j6 candida alb	
269	40	41.2	71	2	Q7MNF6_VIBVY	Q7mnf6 vibrio vuln	342	40	41.2	719	2	Q7FAQ9_ORYSA	Q7faq9 oryza sativ	
270	40	41.2	102	1	YBH1_YEAST	P381B5 saccharomyc	343	40	41.2	727	2	Q9SKW0_ARATH	Q9skw0 arabidopsis	
271	40	41.2	116	1	RNP2_METMA	Q8ptu2 methanosarc	344	40	41.2	731	2	Q9SI25_ARATH	Q9st25 arabidopsis	
272	40	41.2	117	2	Q4N5T3_THEPA	Q4n5t3 theileria p	345	40	41.2	735	2	Q9STZ1_ARATH	Q9stz1 arabidopsis	
273	40	41.2	132	1	RNP2_METAC	Q8tpx3 methanosarc	346	40	41.2	753	2	Q8L741_ARATH	Q8l741 arabidopsis	
274	40	41.2	139	2	Q577X7_BRUAB	Q577x7 brucella ab	347	40	41.2	753	2	Q9LIC9_ARATH	Q9lic9 arabidopsis	
275	40	41.2	139	2	Q8YC43_BRUME	Q8yc43 brucella me	348	40	41.2	764	2	Q4SL31_TETNG	Q4sl31 tetraodon n	
276	40	41.2	142	2	Q65J74_BACLD	Q65j74 bacillus li	349	40	41.2	792	2	Q7SZW1_BRARE	Q7szw1 brachydanio	
277	40	41.2	163	2	Q8YKS7_ANASP	Q8yks7 anabaena sp	350	40	41.2	815	2	Q8C730_MOUSE	Q8c730 mus musculu	
278	40	41.2	167	2	Q82TA8_NITEU	Q82ta8 nitrosomona	351	40	41.2	828	2	Q4RGA8_TETNG	Q4rga8 tetraodon n	
279	40	41.2	208	2	Q221S6_CAEEL	Q221s6 caenorhabdi	352	40	41.2	830	1	CAD16_MOUSE	Q88338 mus musculu	
280	40	41.2	209	2	Q628Y9_CAEBR	Q628y9 caenorhabdi	353	40	41.2	830	2	Q546A8_MOUSE	Q546a8 mus musculu	
281	40	41.2	217	2	Q8EUV8_MYCPE	Q8euv8 mycoplasma	354	40	41.2	876	2	Q4RVH8_TETNG	Q4rvh8 tetraodon n	
282	40	41.2	219	2	Q8ERG6_OCEIH	Q8erg6 oceanobacill	355	40	41.2	879	2	Q6CX10_KLULA	Q6cx10 kluyveromyc	
283	40	41.2	221	2	Q856Q5_9CAUD	Q856q5 mycobacteri	356	40	41.2	888	1	SYA_BARQU	Q6fz1 bartonella	
284	40	41.2	226	2	Q8RHFO_FUSNN	Q8rhfo fusobacteri	357	40	41.2	914	2	Q9SV50_ARATH	Q9sv50 arabidopsis	
285	40	41.2	228	1	CLCB_BOVIN	P04975 bos taurus	358	40	41.2	958	2	Q6KHX7_MYCNO	Q6kxh7 mycoplasma	
286	40	41.2	229	1	CLCB_HUMAN	P04977 homo sapien	359	40	41.2	960	2	Q9M0Q3_ARATH	Q9m0q3 arabidopsis	
287	40	41.2	229	1	CLCB_MOUSE	Q61rux5 mus musculu	360	40	41.2	972	2	Q9LRA1_ARATH	Q9lra1 arabidopsis	
288	40	41.2	229	1	CLCB_RAT	P08082 rattus norv	361	40	41.2	977	1	ZNF31_HUMAN	P17040 homo sapien	
289	40	41.2	231	2	Q19601_CAEEL	Q19601 caenorhabdi	362	40	41.2	977	2	Q5TAY6_HUMAN	Q5tav6 homo sapien	
290	40	41.2	236	1	PUR7_RICPR	Q05946 rickettsia	363	40	41.2	1043	2	Q6ZN23_HUMAN	Q6zn23 homo sapien	
291	40	41.2	236	2	Q68XE9_RICTY	Q68xe9 rickettsia	364	40	41.2	1299	2	Q8JU62_9REOV	Q8ju62 golden shin	
292	40	41.2	239	2	Q4QDM4_LEIMA	Q4qdm4 leishmania	365	40	41.2	1299	2	Q9E3W0_9REOV	Q9e3w0 grass carp	
293	40	41.2	243	2	Q4MTPT_BACCE	Q4mtpt bacillus ce	366	40	41.2	1399	2	Q5XPF9_ARATH	Q5xpf9 arabidopsis	
294	40	41.2	243	2	Q635M7_BACCC	Q635m7 bacillus ce	367	40	41.2	1421	2	Q80907_ARATH	Q80907 arabidopsis	
295	40	41.2	243	2	Q6HEB3_BACHK	Q6heb3 bacillus th	368	40	41.2	1676	2	Q8AG67_BACTN	Q8ag67 bacteroides	
296	40	41.2	243	2	Q81MH6_BACAN	Q81mh6 bacillus an	369	40	41.2	2189	2	Q6JKS5_9ENTO	Q6jks5 human coxa	
297	40	41.2	245	2	Q819D2_BACCR	Q819d2 bacillus ce	370	40	41.2	2446	2	Q7RNH3_PLAYO	Q7rnh3 plasmodium	
298	40	41.2	248	2	Q731P5_BACCI	Q731p5 bacillus ce	371	40	41.2	5147	1	FAT_DROME	P33450 drosophila	
299	40	41.2	271	1	MURI_LACLA	Q9c928 lactococcus	372	39.5	40.7	113	2	Q8SPS0_RABIT	Q8sp50 oryctolagus	
300	40	41.2	294	2	Q5E1S2_VIBF1	Q5e1s2 vibrio fisc	373	39.5	40.7	147	2	Q7Z4F3_HUMAN	Q7z4f3 homo sapien	
301	40	41.2	294	2	Q9YLP3_9ENTO	Q9y1p3 human coxa	374	39.5	40.7	148	2	Q6P7G5_XENLA	Q6p7g5 xenopus lae	
302	40	41.2	310	2	Q7V653_PROMM	Q7v653 prochloroco	375	39.5	40.7	177	1	CAV1_HUMAN	Q03135 homo sapien	
303	40	41.2	313	1	CYF_MESVI	Q9mun6 mesostigma	376	39.5	40.7	178	1	CAV1_BOVIN	P79132 bos taurus	
304	40	41.2	325	2	Q7KTP7_DROME	Q7ktp7 drosophila	377	39.5	40.7	178	1	CAV1_CANFA	P73124 canis fami	
305	40	41.2	327	2	Q93345_CAEEL	Q93345 caenorhabdi	378	39.5	40.7	178	1	CAV1_CHICK	P35431 gallus gall	
306	40	41.2	339	2	Q5GRD6_ALCXX	Q5grd6 alcaligenes	379	39.5	40.7	178	1	CAV1_MOUSE	P49817 mus musculu	
307	40	41.2	343	2	Q8RL38_COMAC	Q8rl38 comamonas a	380	39.5	40.7	178	1	CAV1_PIG	Q6rva9 sus scrofa	
308	40	41.2	352	2	Q4WAM7_ASPTU	Q4wam7 aspergillus	381	39.5	40.7	178	1	CAV1_RAT	P41350 rattus norv	
309	40	41.2	353	2	Q6BGS8_PARTE	Q6bgs8 paramecium	382	39.5	40.7	178	2	Q5PX19_BOVIN	Q5px19 bos taurus	
310	40	41.2	364	2	Q6FV33_CANGA	Q6fv33 candida gla	383	39.5	40.7	178	2	Q6B3Y2_OVIS	Q6b3y2 ovis aries	
311	40	41.2	367	1	ISPG_PASMU	P57987 pasteurella	384	39.5	40.7	180	2	Q5EBF9_XENTR	Q5ebf9 xenopus tro	
312	40	41.2	384	2	Q8ZYW8_PYRAE	Q8zyw8 pyrobaculum	385	39.5	40.7	180	2	Q6IRP8_XENLA	Q6irp8 xenopus lae	
313	40	41.2	419	2	Q7RDG2_PLAYO	Q7rdg2 plasmodium	386	39.5	40.7	217	2	Q59E85_HUMAN	Q59e85 xenopus lae	
314	40	41.2	425	2	Q4XX66_PLACH	Q4xx66 plasmodium	387	39.5	40.7	219	2	Q8JHX1_XENLA	Q8jhx1 xenopus lae	
315	40	41.2	428	2	Q5AZV6_EWENI	Q5azv6 aspergillus	388	39.5	40.7	357	2	Q61DJ7_CAEER	Q61dj7 caenorhabdi	
316	40	41.2	433	2	Q96FA9_HUMAN	Q96fa9 homo sapien	389	39.5	40.7	383	2	Q88MP5_PSEPK	Q88mp5 pseudomonas	
317	40	41.2	433	2	Q5TAY7_HUMAN	Q5tay7 homo sapien	390	39.5	40.7	427	2	Q54NN4_DICDI	Q54nn4 dictyosteli	
318	40	41.2	435	2	Q4Z1H0_PLABE	Q4z1h0 plasmodium	391	39.5	40.7	432	1	IF36_CAEEL	Q61820 caenorhabdi	
319	40	41.2	442	2	Q8E1W6_DICDI	Q8e1w6 dictyosteli	392	39.5	40.7	450	2	Q7Q6X2_ANOGA	Q7q6x2 anopheles g	
320	40	41.2	442	2	Q5E9X8_BOVIN	Q5e9x8 bos taurus	393	39.5	40.7	468	2	Q94JZ8_ARATH	Q94jz8 arabidopsis	
321	40	41.2	454	2	Q4P8T5_USTMA	Q4p8t5 ustilago ma	394	39.5	40.7	514	2	Q9MA26_ARATH	Q9ma26 arabidopsis	
322	40	41.2	469	2	Q8MRQ1_DROME	Q8mrq1 drosophila	395	39.5	40.7	676	2	Q9C2A6_NEUCR	Q9c2a6 neuropesta	
323	40	41.2	473	2	Q727Y8_DESVH	Q727y8 desulfovibr	396	39.5	40.7	1106	2	Q8BX87_MOUSE	Q8bx87 m mus muscu	

397	39.5	40.7	1166	2	Q4RS63	TETNG	Q4rs63	tetraodon n	470	39	40.2	859	2	Q54Y91	DICDI	Q54y91	dictyostelli
398	39	40.2	89	2	Q20941	CABEL	Q20941	caenorhabdi	471	39	40.2	873	2	Q41315	GIBZE	Q41315	gibberella
399	39	40.2	106	2	Q4XC00	PLACH	Q4xc00	plasmidium	472	39	40.2	879	1	PMCI	SCHPO	Q9py74	schizosacch
400	39	40.2	123	2	Q896R7	CLOTE	Q896r7	clostridium	473	39	40.2	898	2	Q60UE2	CABBR	Q60ue2	caenorhabdi
401	39	40.2	124	2	Q84VJ5	ORYSA	Q84vj5	oryza sativ	474	39	40.2	902	1	DSC2	MOUSE	P55292	mus musculus
402	39	40.2	138	2	Q7SX19	BRABE	Q7sx19	brachydanio	475	39	40.2	957	2	Q5U2Z8	XENTR	Q5u2z8	xenopus tro
403	39	40.2	209	2	Q7P831	FUSNV	Q7p831	fusobacteri	476	39	40.2	984	2	Q81PZ2	DROME	Q81p22	drosophila
404	39	40.2	219	2	Q5X1P7	LEGPA	Q5x1p7	legionella	477	39	40.2	1029	2	Q753H8	ASHGO	Q753h8	ashbya goss
405	39	40.2	231	2	Q97EL8	CLOAB	Q97el8	clostridium	478	39	40.2	1087	2	Q619D8	CABBR	Q619d8	caenorhabdi
406	39	40.2	236	1	PUR7	RICCN	Q92ix6	rickettsia	479	39	40.2	1095	1	QDC25	SACKL	Q02342	saccharomyc
407	39	40.2	236	2	Q7PB33	RICSI	Q7pb33	rickettsia	480	39	40.2	1122	2	Q5HAF3	EHRRW	Q5haf3	ehrlichia r
408	39	40.2	243	2	Q6N206	RHOPA	Q6n206	rhodopeudo	481	39	40.2	1123	2	Q5FG85	EHRRG	Q5fg85	ehrlichia r
409	39	40.2	245	2	Q4ZAT9	GVIRU	Q4zat9	bacterioph	482	39	40.2	1196	2	Q9EMY3	AMEPV	Q9emy3	amaecta moo
410	39	40.2	247	2	Q4HCL7	9DEIO	Q4hcl7	deinococcus	483	39	40.2	1251	2	Q6SLD1	COCHE	Q6sld1	cochliobolu
411	39	40.2	258	2	Q5N165	FRAIT	Q5n165	francisella	484	39	40.2	1402	2	Q610A1	CABBR	Q610a1	caenorhabdi
412	39	40.2	261	2	Q6AMY6	DESPS	Q6amy6	desulfotale	485	39	40.2	1512	2	Q5B591	EMENI	Q5b591	aspergillus
413	39	40.2	284	2	Q4NTE7	9DELT	Q4nte7	anaeromyxob	486	39	40.2	1565	2	Q4Q496	LEIMA	Q4q496	leishmania
414	39	40.2	286	2	Q84VQ8	MAIZE	Q84vq8	zea mays (m	487	39	40.2	1599	2	Q5CZH4	PARTE	Q5czh4	paramecium
415	39	40.2	286	2	Q84VQ9	MAIZE	Q84vq9	zea mays (m	488	39	40.2	1745	2	Q4N6X8	THEPA	Q4n6x8	theileria p
416	39	40.2	288	2	Q8GWB4	ARATH	Q8gwb4	arabidopsis	489	39	40.2	1917	2	Q4N6V7	THEPA	Q4n6v7	theileria p
417	39	40.2	288	2	Q6MI74	BDEBA	Q6mi74	bdellovibri	490	39	40.2	2628	2	Q7S0T8	NEUCR	Q7s0t8	neurospora
418	39	40.2	297	1	HIS1	KJULA	Q6cid6	kluyveromyc	491	39	40.2	3228	2	Q5CL19	CRYHO	Q5cl19	cryptospori
419	39	40.2	297	2	Q7NA38	PHOLL	Q7na38	photorhabdu	492	39	40.2	3229	2	Q5CXF3	CRYPV	Q5cxp3	cryptospori
420	39	40.2	299	2	Q4YV07	PLABE	Q4yv07	plasmodium	493	39	40.2	3316	2	Q8VQF8	XENBV	Q8vqf8	xenorhabdus
421	39	40.2	303	2	Q54R44	DICDI	Q54r44	dictyosteli	494	38.5	39.7	113	2	Q53777	STAAU	Q53777	staphylococ
422	39	40.2	307	2	Q89D87	BRABA	Q89d87	bradyrhizob	495	38.5	39.7	124	2	Q53600	STAAU	Q53600	staphylococ
423	39	40.2	317	2	Q7V2L5	PROMP	Q7v2l5	prochloroco	496	38.5	39.7	124	2	Q7A732	STAAU	Q7a732	staphylococ
424	39	40.2	320	1	CYF	PORPU	P51265	porphyra pu	497	38.5	39.7	124	2	Q7A2W5	STAAU	Q7a2w5	staphylococ
425	39	40.2	330	2	Q52B03	MAGGR	Q52b03	magnaporthe	498	38.5	39.7	124	2	Q7A1N5	STAAU	Q7a1n5	staphylococ
426	39	40.2	335	1	TAGH	LISIN	Q92cv8	listeria in	499	38.5	39.7	124	2	Q6GJ52	STAAU	Q6gj52	staphylococ
427	39	40.2	340	2	Q6MKW2	BDEBA	Q6mkw2	bdellovibri	500	38.5	39.7	124	2	Q6GBL2	STAAU	Q6gbl2	staphylococ
428	39	40.2	342	2	Q4W9F9	ASPFU	Q4w9f9	aspergillus									
429	39	40.2	353	2	Q8YN48	ANASP	Q8yn48	anabaena sp									
430	39	40.2	377	2	Q6QW87	AZOB	Q6qw87	azospirillu									
431	39	40.2	379	2	Q8PZS1	METWA	Q8pzs1	methanosarc									
432	39	40.2	381	2	Q9K9F9	BACHD	Q9k9f9	bacillus ha									
433	39	40.2	385	2	Q56610	XENTR	Q56610	xenopus tro									
434	39	40.2	392	2	Q4UNW5	XANCP	Q4unw5	xanthomonas									
435	39	40.2	392	2	Q8P7G4	XANCP	Q8p7g4	xanthomonas									
436	39	40.2	398	2	Q4UWU1	XANCP	Q4uwu1	xanthomonas									
437	39	40.2	398	2	Q8P791	XANCP	Q8p791	xanthomonas									
438	39	40.2	426	2	Q8NA62	HUMAN	Q8na62	homo sapien									
439	39	40.2	436	2	Q4N111	THEPA	Q4n111	theileria p									
440	39	40.2	442	2	Q7UY13	RHOPA	Q7uy13	rhodopirell									
441	39	40.2	459	2	Q86TL5	HUMAN	Q86tl5	homo sapien									
442	39	40.2	460	2	Q4UEJ1	THEAN	Q4uej1	theliceria a									
443	39	40.2	461	1	TRME	HELPU	Q9zjg6	helicobacte									
444	39	40.2	461	1	TRME	HELPU	Q25991	helicobacte									
445	39	40.2	499	2	Q6YRB9	ONYPE	Q6yrb9	onion yello									
446	39	40.2	530	2	Q51T62	MAGR	Q51t62	magnaporthe									
447	39	40.2	532	2	Q00069	ASCIM	Q00069	ascobolus i									
448	39	40.2	569	2	Q81YW6	HUMAN	Q81yw6	homo sapien									
449	39	40.2	577	2	Q87AA1	XYLFT	Q87aa1	xyella fas									
450	39	40.2	577	2	Q9PAH4	XYLFA	Q9pah4	xyella fas									
451	39	40.2	584	2	Q55449	SYNV3	Q55449	synchocyst									
452	39	40.2	588	2	Q9A696	CAUCR	Q9a696	caulobacter									
453	39	40.2	600	2	Q6KHD3	MYCWO	Q6khd3	mycoplasma									
454	39	40.2	682	2	Q5A3Q5	CANAL	Q5a2q5	candida alb									
455	39	40.2	726	1	RNR	MYCPN	P75529	mycoplasma									
456	39	40.2	743	2	Q6FQ11	CANGA	Q6fq11	candida gla									
457	39	40.2	753	2	Q80VY6	MOUSE	Q80vy6	mus musculu									
458	39	40.2	755	2	Q851U2	ORYSA	Q851u2	oryza sativ									
459	39	40.2	808	2	Q5CF11	CRYPV	Q5cf11	cryptospori									
460	39	40.2	811	1	DRL30	ARATH	Q91z55	arabidopsis									
461	39	40.2	818	2	Q55FAB	DICDI	Q55fab	dictyosteli									
462	39	40.2	821	2	Q8BRE1	MOUSE	Q8bre1	mus musculu									
463	39	40.2	822	1	CADH3	MOUSE	P10287	mus musculu									
464	39	40.2	822	2	Q8BSL6	MOUSE	Q8bsl6	mus musculu									
465	39	40.2	833	2	Q8TCR3	HUMAN	Q8tcr3	homo sapien									
466	39	40.2	833	2	Q96SP7	HUMAN	Q96sp7	homo sapien									
467	39	40.2	848	2	Q544V1	MOUSE	Q544v1	m 11 days p									
468	39	40.2	848	2	Q6PEU5	MOUSE	Q6peu5	mus musculu									
469	39	40.2	855	2	Q9COH1	HUMAN	Q9coh1	homo sapien									

RESULT 1

DSG3 CANFA

ID_DSG3_CANFA

AC Q7YRU7;

DT 10-MAY-2005 (Rel. 47, Created)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Desmoglein-3 precursor.

GN Name=DSG3;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

OC Canis.

OX NCBI_TaxID=9615;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUES=Oral mucosa;

RX MEDLINE=228710058; PubMed=14507443; DOI=10.1016/S0923-1811(03)00095.1;

RT Nishifuji K., Anagai M., Ota T., Nishikawa T., Iwasaki T.;

RT "Cloning of canine desmoglein 3 and immunoreactivity of serum

RT antibodies in human and canine pemphigus vulgaris with its

RT extracellular domains.";

RL J. Dermatol. Sci. 32:181-191(2003).

CC -!- FUNCTION: Component of intercellular desmosome junctions. Involved

CC in the interaction of plaque proteins and intermediate filaments

CC mediating cell-cell adhesion (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- DOMAIN: Calcium may be bound by the cadherin-like repeats

CC (Potential).

CC -!- SIMILARITY: Contains 4 cadherin domains.

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CC use as long as its content is in no way modified and this statement is not

CC removed.

CC

CC

ALIGNMENTS

ALIGNMENTS

RESULT 1

DSG3	CANFA	STANDARD	PRT	993 AA.
ID	DSG3	CANFA	STANDARD	PRT
AC	Q7YRU7			
DT	10-MAY-2005 (Rel. 47, Created)			
DT	10-MAY-2005 (Rel. 47, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Desmoglein-3 precursor.			
GN	Name=DSG3;			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Canidae;			
OC	Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RC	TISSUE=Oral mucosa;			
RX	MEDLINE=22871058; PubMed=14507443; DOI=10.1016/S0923-1811(03)00095.1;			
RA	Nishifuji K., Amagai M., Ota T., Nishikawa T., Iwasaki T.;			
RT	Cloning of canine desmoglein 3 and immunoreactivity of serum			
RT	antibodies in human and canine pemphigus vulgaris with its			
RT	extracellular domains.;			
RL	J. Dermatol. Sci. 32:181-191(2003).			
CC	-!- FUNCTION: Component of intercellular desmosome junctions. Involved			
CC	in the interaction of plaque proteins and intermediate filaments			
CC	mediating cell-cell adhesion (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-!- DOMAIN: Calcium may be bound by the cadherin-like repeats			
CC	(potential).			
CC	-!- SIMILARITY: Contains 4 cadherin domains.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is			
CC	removed.			
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OM protein - protein search, using sw model

Run on: .November 26, 2005, 01:31:04 ; Search time 46 Seconds
(without alignments)
34.149 Million cell updates

Title: US-10-799-005A-1

Perfect score:

Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

scoring cable: BLOSUM62
Gapop 10.0 , Gapext 0.5

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ALIGNMENTS

RESULT 1

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; Sequence 8229, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8229
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8229

Query Match 100.0%; Score 97; DB 2; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2,1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 201 EPNHLSKIAFKIVSQEPA 219

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Title: US-10-799-005A-1

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Listing first 500 summaries

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SUMMARIES

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98	48	49.5	807	4	US-10-232-233-188	Sequence 188, App
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263	48	49.5	807	4	US-10-063-587-98	Sequence 98, Appl	336	48	49.5	807	4	US-10-063-618-98	Sequence 98, Appl
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412	41	42.3	65	4	US-10-001-883-136	Sequence 136, App	485	39	40.2	426	4	US-10-104-047-3436	Sequence 3436, Ap
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/10799005A
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; GENERAL INFORMATION:
; APPLICANT: Rasmussen, James
; APPLICANT: Yu, Bei
; TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
; TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASES
; FILE REFERENCE: PEPT-P01-005
; CURRENT APPLICATION NUMBER: US/10/799,005A
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from human desmoglein 3
; OTHER INFORMATION: protein
US-10-799-005A-1

Query Match 100.0%; Score 97; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPNHLSKIAFKIVSOEPA 19

Db 1 EPNHLSKIAFKIVSOEPA 19

RESULT 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:42:05 ; Search time 9 Seconds
(without alignments)
6.399 Million cell updates/sec

Title: US-10-799-005a-1

Perfect score: 97
Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pdb:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pdb:*
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7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pdb:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	42.3	301	1	US-10-793-626-1826
2	38	39.2	392	1	US-10-957-569-35
3	36	37.1	445	7	US-11-082-389-376
4	36	37.1	745	1	US-10-793-626-1742
5	35	36.1	247	1	US-10-510-386-242
6	35	36.1	572	1	US-10-793-626-2974
7	34	35.1	205	1	US-10-131-826A-274
8	34	35.1	266	1	US-10-793-626-1974
9	34	35.1	903	7	US-11-057-058-65
10	33	34.0	161	1	US-10-793-626-842
11	33	34.0	309	1	US-10-793-626-936
12	33	34.0	392	1	US-10-793-626-1008
13	33	34.0	500	1	US-10-957-569-18
14	32.5	33.5	220	7	US-11-082-389-72
15	32.5	33.5	421	7	US-11-082-389-70
16	32	33.0	111	1	US-10-845-413-75
17	32	33.0	195	1	US-10-793-626-2120
18	32	33.0	258	1	US-10-793-626-666
19	32	33.0	339	1	US-10-485-517-367
20	32	33.0	411	7	US-11-061-869-12
21	32	33.0	565	1	US-10-793-626-2608
22	32	33.0	645	1	US-10-793-626-1770
23	32	33.0	1059	7	US/11/062
24	32	33.0	1084	7	US/11/062
25	32	33.0	1145	1	US-10-793-626-1432

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Sequence 3038, Ap

99	29	29.9	159	1	US-10-689-742-130	Sequence 130, App	172	28	28.9	1	US-10-793-626-2690	Sequence 2690, App	
100	29	29.9	204	1	US-10-793-626-692	Sequence 692, App	173	28	28.9	199	1	US-10-793-626-146	Sequence 146, App
101	29	29.9	269	1	US-10-793-626-1158	Sequence 1158, App	174	28	28.9	241	1	US-10-510-386-104	Sequence 104, App
102	29	29.9	271	1	US-10-793-626-314	Sequence 314, App	175	28	28.9	252	1	US-10-821-234-1304	Sequence 1304, App
103	29	29.9	277	1	US-10-793-626-2178	Sequence 2178, App	176	28	28.9	299	1	US-10-793-626-1888	Sequence 1888, App
104	29	29.9	279	1	US-10-793-626-858	Sequence 858, App	177	28	28.9	299	1	US-10-793-626-2798	Sequence 2798, App
105	29	29.9	289	1	US-10-793-626-3254	Sequence 3254, App	178	28	28.9	302	1	US-10-793-626-1652	Sequence 1652, App
106	29	29.9	341	1	US-10-793-626-3248	Sequence 3248, App	179	28	28.9	304	1	US-10-793-626-2450	Sequence 2450, App
107	29	29.9	362	7	US-11-012-762-30	Sequence 30, Appl	180	28	28.9	311	1	US-10-793-626-2450	Sequence 184, App
108	29	29.9	362	7	US-11-012-762-32	Sequence 32, Appl	181	28	28.9	331	1	US-10-131-826A-162	Sequence 162, App
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110	29	29.9	367	1	US-10-821-234-1569	Sequence 1569, App	183	28	28.9	372	1	US-10-131-826A-106	Sequence 106, App
111	29	29.9	368	7	US-11-082-389-320	Sequence 320, App	184	28	28.9	377	1	US-10-821-234-1436	Sequence 1436, App
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113	29	29.9	379	1	US-10-793-626-2810	Sequence 2810, App	186	28	28.9	386	7	US-11-012-762-44	Sequence 44, Appl
114	29	29.9	380	1	US-10-793-626-702	Sequence 702, App	187	28	28.9	389	1	US-10-980-388-116	Sequence 116, App
115	29	29.9	441	1	US-10-821-234-1668	Sequence 1668, App	188	28	28.9	416	1	US-10-821-234-1375	Sequence 1375, App
116	29	29.9	643	7	US-11-074-176-318	Sequence 318, App	189	28	28.9	423	1	US-10-467-962B-85	Sequence 85, Appl
117	29	29.9	664	1	US-10-485-517-308	Sequence 308, App	190	28	28.9	429	1	US-10-793-626-3174	Sequence 3174, App
118	29	29.9	667	7	US-11-074-176-64	Sequence 64, Appl	191	28	28.9	433	1	US-10-821-234-1353	Sequence 1353, App
119	29	29.9	877	7	US-11-074-176-322	Sequence 322, App	192	28	28.9	469	1	US-10-821-234-1151	Sequence 1151, App
120	29	29.9	883	7	US-11-074-176-88	Sequence 88, Appl	193	28	28.9	525	7	US-11-074-176-146	Sequence 146, App
121	29	29.9	895	1	US-10-485-517-129	Sequence 129, App	194	28	28.9	534	1	US-10-821-234-1341	Sequence 1341, App
122	29	29.9	1065	1	US-10-793-626-1212	Sequence 1212, App	195	28	28.9	644	1	US-10-821-234-1107	Sequence 1107, App
123	29	29.9	1150	1	US-10-821-234-1083	Sequence 1083, App	196	28	28.9	708	1	US-10-131-826A-298	Sequence 298, App
124	29	29.9	1176	1	US-10-821-234-897	Sequence 897, App	197	28	28.9	746	1	US-10-793-626-652	Sequence 652, App
125	29	29.9	1263	1	US-10-485-517-127	Sequence 127, App	198	28	28.9	754	1	US-10-793-626-1296	Sequence 1296, App
126	29	29.9	1304	1	US-10-821-234-1648	Sequence 1648, App	199	28	28.9	812	7	US-11-010-874-1	Sequence 1, Appl
127	29	29.9	1637	1	US-10-821-234-1283	Sequence 1283, App	200	28	28.9	820	1	US-10-821-234-1176	Sequence 1176, App
128	29	29.9	1671	1	US-10-821-234-1204	Sequence 1204, App	201	28	28.9	943	1	US-10-821-234-1012	Sequence 1012, App
129	29	29.9	2280	7	US-11-022-562-211	Sequence 211, App	202	28	28.9	1006	1	US-10-793-626-154	Sequence 154, App
130	29	29.9	2314	7	US-11-013-759-11	Sequence 11, Appl	203	28	28.9	1070	7	US-11/062	Sequence 4, Appl
131	29	29.9	2384	1	US-10-821-234-1545	Sequence 1545, App	204	28	28.9	1095	7	US-11/062	Sequence 7, Appl
132	28.5	29.4	229	1	US-10-510-386-228	Sequence 228, App	205	28	28.9	1142	7	US-11-109-156-22	Sequence 22, Appl
133	28.5	29.4	296	1	US-10-793-626-1674	Sequence 1674, App	206	28	28.9	1169	7	US-11-077-550-20	Sequence 20, Appl
134	28.5	29.4	428	1	US-10-793-626-266	Sequence 266, App	207	28	28.9	1463	1	US-10-971-982-3	Sequence 3, Appl
135	28.5	29.4	873	1	US-10-793-626-3036	Sequence 3036, App	208	28	28.9	1614	1	US-10-821-234-903	Sequence 903, App
136	28.5	29.4	886	1	US-10-821-234-1329	Sequence 1329, App	209	28	28.9	1827	7	US-11-057-058-62	Sequence 62, Appl
137	28.5	29.4	903	1	US-10-689-742-142	Sequence 142, App	210	28	28.9	2323	1	US-10-793-626-760	Sequence 760, App
138	28.5	29.4	904	1	US-10-967-648A-14	Sequence 14, Appl	211	28	28.9	2516	1	US-10-647-956A-2	Sequence 2, Appl
139	28.5	29.4	1275	1	US-10-821-234-1598	Sequence 1598, App	212	27.5	28.4	76	1	US-10-510-880-6	Sequence 6, Appl
140	28	28.9	89	7	US-11-053-076-35	Sequence 35, Appl	213	27.5	28.4	76	1	US-10-977-334-2	Sequence 2, Appl
141	28	28.9	100	1	US-10-793-626-2158	Sequence 2158, App	214	27.5	28.4	108	1	US-10-510-880-5	Sequence 5, Appl
142	28	28.9	107	1	US-10-845-413-287	Sequence 287, App	215	27.5	28.4	108	1	US-10-875-800-1	Sequence 1, Appl
143	28	28.9	107	1	US-10-845-413-288	Sequence 288, App	216	27.5	28.4	134	1	US-10-510-880-1	Sequence 1, Appl
144	28	28.9	107	1	US-10-845-413-290	Sequence 290, App	217	27.5	28.4	134	1	US-10-875-800-2	Sequence 2, Appl
145	28	28.9	107	1	US-10-845-413-307	Sequence 307, App	218	27.5	28.4	362	1	US-10-793-626-3120	Sequence 3120, App
146	28	28.9	111	1	US-10-845-413-66	Sequence 66, Appl	219	27.5	28.4	614	1	US-10-821-234-1041	Sequence 1041, App
147	28	28.9	111	1	US-10-845-413-79	Sequence 79, Appl	220	27	27.8	14	1	US-10-989-226-1	Sequence 1, Appl
148	28	28.9	113	1	US-10-845-413-85	Sequence 85, Appl	221	27	27.8	19	1	US-10-503-575-117	Sequence 117, App
149	28	28.9	113	1	US-10-845-413-88	Sequence 88, Appl	222	27	27.8	40	1	US-10-516-768-6	Sequence 6, Appl
150	28	28.9	113	1	US-10-845-413-91	Sequence 91, Appl	223	27	27.8	67	7	US-11-074-176-302	Sequence 302, App
151	28	28.9	113	1	US-10-845-413-96	Sequence 96, Appl	224	27	27.8	79	1	US-10-689-742-194	Sequence 194, App
152	28	28.9	113	1	US-10-845-413-281	Sequence 281, App	225	27	27.8	83	1	US-10-131-826A-440	Sequence 440, App
153	28	28.9	113	1	US-10-845-413-282	Sequence 282, App	226	27	27.8	111	1	US-10-793-626-384	Sequence 384, App
154	28	28.9	113	1	US-10-845-413-284	Sequence 284, App	227	27	27.8	113	1	US-10-845-413-280	Sequence 280, App
155	28	28.9	113	1	US-10-845-413-291	Sequence 291, App	228	27	27.8	113	1	US-10-845-413-283	Sequence 283, App
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167	28	28.9	135	1	US-10-793-626-1106	Sequence 1106, App	240	27	27.8	113	1	US-10-845-413-310	Sequence 310, App
168	28	28.9	159	1	US-10-793-626-878	Sequence 878, App	241	27	27.8	113	1	US-10-845-413-311	Sequence 311, App
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171	28	28.9	189	1	US-10-793-626-1998	Sequence 1998, App	244	27	27.8	123	1	US-10-793-626-56	Sequence 56, Appl

245	27	27.8	125	1	US-10-516-768-8	Sequence 8, Appli	318	27	27.8	1213	7	US-11-074-176-256	Sequence 256, App
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247	27	27.8	138	1	US-10-793-626-1540	Sequence 1540, Ap	320	27	27.8	1302	7	US-11-004-057-6	Sequence 6, Appli
248	27	27.8	140	1	US-10-793-626-1256	Sequence 1256, Ap	321	27	27.8	1493	7	US-11-004-057-4	Sequence 4, Appli
249	27	27.8	145	1	US-10-793-626-2328	Sequence 2328, Ap	322	27	27.8	1493	7	US-11-004-057-21	Sequence 21, Appli
250	27	27.8	146	1	US-10-131-826A-408	Sequence 408, App	323	27	27.8	1857	7	US-11-057-058-60	Sequence 60, Appli
251	27	27.8	176	1	US-10-793-626-612	Sequence 612, App	324	27	27.8	1857	7	US-11-057-058-61	Sequence 61, Appli
252	27	27.8	180	1	US-10-510-386-144	Sequence 144, App	325	27	27.8	1897	7	US-10-821-234-1635	Sequence 1635, Ap
253	27	27.8	190	1	US-10-466-794A-6	Sequence 6, Appli	326	27	27.8	2053	7	US-11-013-759-9	Sequence 9, Appli
254	27	27.8	210	1	US-11-038-284-24	Sequence 24, Appli	327	27	27.8	2647	1	US-10-821-234-1303	Sequence 1303, Ap
255	27	27.8	222	1	US-10-793-626-1510	Sequence 1510, Ap	328	27	27.8	3056	7	US-11-109-156-20	Sequence 20, Appli
256	27	27.8	236	1	US-11-140-965-4	Sequence 4, Appli	329	26.5	27.3	40	1	US-10-552-535A-36	Sequence 36, Appli
257	27	27.8	245	1	US-10-131-826A-214	Sequence 214, App	330	26.5	27.3	164	1	US-10-793-626-252	Sequence 252, App
258	27	27.8	251	1	US-10-793-626-3050	Sequence 3050, Ap	331	26.5	27.3	212	1	US-10-793-626-1622	Sequence 1622, Ap
259	27	27.8	256	1	US-11-179-977-2	Sequence 2, Appli	332	26.5	27.3	227	1	US-10-977-334-7	Sequence 7, Appli
260	27	27.8	258	7	US-11-038-742-23	Sequence 23, Appli	333	26.5	27.3	249	1	US-10-793-626-306	Sequence 306, App
261	27	27.8	291	1	US-10-689-742-23	Sequence 23, Appli	334	26.5	27.3	249	1	US-10-793-626-776	Sequence 776, App
262	27	27.8	294	1	US-10-793-626-2346	Sequence 2346, Ap	335	26.5	27.3	309	1	US-10-793-626-648	Sequence 648, App
263	27	27.8	295	1	US-10-793-626-2998	Sequence 2998, Ap	336	26.5	27.3	324	1	US-10-793-626-2674	Sequence 2674, Ap
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267	27	27.8	322	1	US-10-689-742-46	Sequence 46, Appli	340	26.5	27.3	495	1	US-10-821-234-1154	Sequence 1154, Ap
268	27	27.8	323	1	US-10-821-234-981	Sequence 981, App	341	26.5	27.3	604	1	US-10-793-626-390	Sequence 390, App
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270	27	27.8	383	1	US-10-793-626-3332	Sequence 3332, Ap	343	26	26.8	86	7	US-10-516-768-30	Sequence 30, Appli
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273	27	27.8	401	1	US-10-793-626-836	Sequence 836, App	346	26	26.8	39	1	US-10-516-768-3	Sequence 3, Appli
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277	27	27.8	428	7	US-11-074-176-344	Sequence 344, App	350	26	26.8	91	1	US-11-053-076-209	Sequence 209, App
278	27	27.8	433	1	US-10-652-893-4	Sequence 4, Appli	351	26	26.8	99	1	US-10-793-626-2484	Sequence 2484, Ap
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280	27	27.8	433	7	US-11-074-176-162	Sequence 162, App	353	26	26.8	101	1	US-10-793-626-1672	Sequence 1672, Ap
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ALIGNMENTS

RESULT 1

US-10-793-626-1826

; Sequence 1826, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; APPLICANT: KIMBERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: P034800S

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1826

; LENGTH: 301

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-10-793-626-1826

Query Match 42.3%; Score 41; DB 1; Length 301;

Best Local Similarity 43.8%; Pred. No. 1.3;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 PNHLSKIAFKIVSQE 17

Db 99 PNHVNSNIHALTASE 114

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:44:55 ; Search time 183 Seconds
(without alignments)
45.619 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 843338

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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9: Geneseq20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	71	73.2	15	AAW64815	Aaw64815 Desmoglei
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4	71	73.2	15	AAW33625	Aab33625 MHC class
5	71	73.2	15	AAG93721	Aag93721 Human des
6	71	73.2	15	AAO17033	Aao17033 Desmoglei
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70	27	27.8	14	9	ADY96447	Ady96447 PET-speci
71	27	27.8	14	9	AEA47658	Aea47658 PET-speci
72	27	27.8	15	5	ABP55461	Abp55461 Human zin
73	27	27.8	15	8	ADJ79714	Adj79714 Human Bra
74	27	27.8	15	8	ADJ79662	Adj79662 Human Bra
75	27	27.8	15	8	ADL26185	Adl26185 Synthetic
76	27	27.8	15	8	ADL26186	Adl26186 Synthetic
77	27	27.8	15	8	ADL26205	Adl26205 Synthetic
78	27	27.8	15	8	ADL26204	Adl26204 Synthetic
79	27	27.8	15	9	ADV55855	Adv55855 G protein
80	27	27.8	15	9	ADV55386	Adv55386 G protein
81	27	27.8	15	9	ADM90243	Adm90243 SARS anti
82	27	27.8	15	9	ADM90244	Adm90244 SARS anti
83	27	27.8	15	9	ADM90632	Adm90632 SARS anti
84	27	27.8	15	9	ADM90241	Adm90241 SARS anti
85	27	27.8	15	9	ADM90629	Adm90629 SARS anti
86	27	27.8	15	9	ADM90630	Adm90630 SARS anti
87	27	27.8	15	9	ADM90631	Adm90631 SARS anti
88	27	27.8	15	9	ADM98850	Adm98850 SARS anti
89	27	27.8	15	9	ADM98851	Adm98851 SARS anti
90	27	27.8	15	9	ADM90245	Adm90245 SARS anti
91	27	27.8	15	9	ADM98952	Adm98952 SARS anti
92	27	27.8	15	9	ADM90633	Adm90633 SARS anti
93	27	27.8	15	9	ADM90242	Adm90242 SARS anti
94	27	27.8	17	2	AAW22728	Aaw22728 Membrane
95	27	27.8	17	4	AAW99425	Aaw99425 Staphylok
96	27	27.8	17	5	AAE20717	Aae20717 Human Mls
97	27	27.8	17	5	AAE21018	Aae21018 Human Icr

98 27 27.8 18 8 ADR84149
 99 27 27.8 19 2 AAY50599 Resin bou
 100 27 27.8 19 7 ADF14612 Rheumatol

ALIGNMENTS

RESULT 1
 AAW04843
 ID AAW04843 standard; peptide; 15 AA.
 AC AAW04843;
 XX
 XX 18-FEB-1997 (first entry)
 XX
 DE Self epitope of desmoglein 3, implicated in autoimmune disease.
 DE
 XX
 XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
 KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
 KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
 KW phosphonannomutase; human papillomavirus; Epstein-Barr virus;
 KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
 XX
 XX Homo sapiens.
 XX
 XX WO9627387-A1.
 PN
 XX
 PD 12-SEP-1996.
 XX
 XX 07-MAR-1996; 96WO-US003182.
 XX
 XX 07-MAR-1995; 95US-00400796.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Strominger JL, Wucherpfennig KW;
 PI
 XX WPI; 1996-425218/42.
 DR
 XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
 PT - useful in disease treatment, and method for identification of other
 PT self and non-self antigens implicated in auto-immune disease.
 XX
 PS Claim 1; Page 39; 58pp; English.
 XX
 CC Pharmaceutical preparations for tolerisation to antigens comprise either
 CC an isolated human non-collagen or non-mysin basic protein (MBP)
 CC polypeptide which is capable of tolerising an individual to an
 CC autoantigen, or an isolated human pathogen polypeptide capable of
 CC tolerising an individual to that polypeptide. In both cases, the
 CC polypeptide (whether self or non-self) includes an amino acid sequence
 CC corresponding to a sequence motif for a MHC class II protein, such as HLA
 CC -DR, which is associated with a human autoimmune disease and which binds
 CC to the polypeptide to activate autoreactive T-cells in individuals with
 CC the autoimmune disease. This peptide is derived from the human desmoglein
 CC 3 protein (amino acids 190-204) and is implicated as a self epitope in
 CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
 CC are described in AAW04841-47
 XX
 SQ Sequence 15 AA;

Query Match 73.2%; Score 71; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAPKIVSQEPA 19
 Db 1 LNSKIAPKIVSQEPA 15

RESULT 2
 AAW64815

ID AAW64815 standard; peptide; 15 AA.
 XX
 AC AAW64815;
 XX
 XX 29-SEP-1998 (first entry)
 XX
 DE Desmoglein-3 190-204.
 DE
 XX
 KW Desmoglein; DG; gene therapy; pemphigus vulgaris; microparticle;
 KW autoantigen; autoimmune disease; MHC.
 XX
 OS Homo sapiens.
 XX
 PN US5783567-A.
 XX
 PD 21-JUL-1998.
 XX
 XX 22-JAN-1997; 97US-00787547.
 PF
 XX 22-JAN-1997; 97US-00787547.
 PR
 XX (PANG-) PANGAEA PHARM INC.
 PA
 XX Langer RS, Hedley ML, Curley JM;
 PI
 XX WPI; 1998-427077/36.
 DR
 XX
 PT Microparticle encapsulated nucleic acids - for recombinant expression of
 PT proteins e.g. in gene therapy.
 PT
 PS Disclosure; Col 4; 42pp; English.
 XX
 CC The patent describes a new preparation of microparticles each comprising
 CC a polymeric matrix and a nucleic acid. The polymeric matrix consists of
 CC one or more synthetic polymers having a solubility in water of less than
 CC 1 mg/l (e.g. poly-lactic-co-glycolic acid); and at least 90% of the
 CC microparticles have a diameter of less than 100 microns. The
 CC microparticles are useful for the delivery of nucleic acids to phagocytic
 CC cells. In one embodiment the microparticles are less than 20 microns in
 CC diameter and the nucleic acid (preferably in closed circular form)
 CC includes an expression control sequence operatively linked to a coding
 CC sequence, where the expression product of the coding sequence is a
 CC polypeptide having a length and a sequence which permits it to bind to an
 CC MHC class I or II molecule. The expression product is thus an effective
 CC stimulator of an immune response in mammals. The present sequence, an
 CC antigenic portion of desmoglein 3, is an example of an MHC class II
 CC peptide which can be expressed by the nucleic acid. It is associated with
 CC pemphigus vulgaris
 XX
 SQ Sequence 15 AA;
 Query Match 73.2%; Score 71; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LNSKIAPKIVSQEPA 19
 Db 1 LNSKIAPKIVSQEPA 15
 RESULT 3
 AAW78814
 ID AAW78814 standard; peptide; 15 AA.
 XX
 AC AAW78814;
 XX
 XX 17-NOV-1998 (first entry)
 DT
 XX Desmoglein 3 protein fragment 190-204.
 DE
 XX
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.

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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:45:55 ; Search time 38 Seconds
(without alignments)
48.108 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	26.8	17	2	PH1822
2	25	25.8	10	2	S66458
3	25	25.8	15	2	S43321
4	23	23.7	14	2	A49018
5	23	23.7	17	2	PC2196
6	22	22.7	9	2	JP0073
7	22	22.7	10	2	F44644
8	22	22.7	13	2	E39778
9	22	22.7	13	2	G44644
10	22	22.7	16	2	Q0RT
11	22	22.7	16	2	PL0124
12	21.5	22.2	19	2	A37968
13	21	21.6	7	2	A15398
14	20	20.6	13	2	JQ2309
15	20	20.6	13	2	JQ2319
16	20	20.6	14	2	PH0795
17	20	20.6	14	2	PH0776
18	20	20.6	15	2	PA0097
19	20	20.6	16	2	PH0777
20	20	20.6	18	2	C40433
21	20	20.6	18	2	S70611
22	19.5	20.1	17	2	C43599
23	19	19.6	12	2	S71034
24	19	19.6	12	2	F84132
25	19	19.6	13	2	S57571
26	19	19.6	13	2	F42762
27	19	19.6	13	2	PC1008
28	19	19.6	13	2	A86126
29	19	19.6	15	2	PS0452

30	19	19.6	15	2	A26212	carboxypeptidase B
31	19	19.6	19	2	C40634	orf21 5' of eryk -
32	18	18.6	9	2	S70345	amine oxidase [cop
33	18	18.6	10	2	PT0309	Ig heavy chain CRD
34	18	18.6	10	2	A24407	amicyanin - Paraco
35	18	18.6	11	2	E60891	phycobilisome 8K 1
36	18	18.6	12	2	D28551	hypothetical prote
37	18	18.6	12	2	A35585	cytokinin-binding
38	18	18.6	12	2	S27024	Na+/K+-exchanging
39	18	18.6	14	2	B29743	translatation initia
40	18	18.6	14	2	PH0801	T-cell receptor al
41	18	18.6	15	2	PQ0174	stylar glycoprotei
42	18	18.6	15	2	PS0251	15K protein 5106 -
43	18	18.6	15	2	A36315	recycling receptor
44	18	18.6	15	2	PH0760	T-cell receptor be
45	18	18.6	15	2	PA0054	protein QF200017 -
46	18	18.6	15	2	A32971	heparin-binding le
47	18	18.6	15	2	S03955	acidic fibroblast
48	18	18.6	15	2	PN0118	hemoglobin beta ch
49	18	18.6	15	4	I38031	hypothetical MN1/T
50	18	18.6	16	2	S51610	hypothetical prote
51	18	18.6	16	2	A49255	T-cell receptor be
52	18	18.6	16	2	PH0759	T-cell receptor be
53	18	18.6	16	2	S13898	alkaline phosphata
54	18	18.6	17	2	S66198	alcohol dehydrogen
55	18	18.6	17	2	I55226	myosin heavy chain
56	18	18.6	17	2	JP0068	ribosomal protein
57	18	18.6	17	2	PH1802	T cell receptor al
58	18	18.6	17	2	S47201	T-cell receptor J-
59	18	18.6	17	2	S05033	photosystem II pro
60	18	18.6	17	2	S59512	probable integrin
61	18	18.6	18	2	A42576	steroid receptor c
62	18	18.6	18	2	I55453	zinc finger homeod
63	18	18.6	18	2	PH1815	T cell receptor al
64	18	18.6	18	2	T13132	protein gp45.1 - p
65	18	18.6	19	2	A41299	T-cell receptor al
66	18	18.6	19	2	S00495	hemocyanin chain I
67	18	18.6	19	2	S63505	63K protein - Euba
68	18	18.6	19	2	S43045	translation elonga
69	17.5	18.0	15	2	PT0222	Ig heavy chain CDR
70	17	17.5	3	3	A33802	thyrotropin-releas
71	17	17.5	8	2	A31570	angiotensin-conver
72	17	17.5	10	2	B39308	glycine reductase
73	17	17.5	10	2	PH0807	T-cell receptor al
74	17	17.5	11	2	G61497	seed protein ws-23
75	17	17.5	12	2	A55837	5-aminimidazole r
76	17	17.5	13	2	H64124	hypothetical prote
77	17	17.5	13	2	A54326	glandular kallikre
78	17	17.5	13	2	PL0157	Ig kappa chain V-I
79	17	17.5	13	2	S47358	T-cell antigen rec
80	17	17.5	13	2	B56864	dipeptidyl-peptida
81	17	17.5	13	2	A59387	VCAM-1 5'UTR bindi
82	17	17.5	14	2	S35267	acetyl-CoA carboxy
83	17	17.5	14	2	PH0516	insulin-like growt
84	17	17.5	15	2	S65717	prostaglandin D-sy
85	17	17.5	15	2	PA0046	protein QA100044 -
86	17	17.5	15	2	S51735	T-cell receptor be
87	17	17.5	15	2	PH0782	T-cell receptor al
88	17	17.5	15	2	I50503	agrin - electric r
89	17	17.5	15	2	S77987	cytochrome-c oxida
90	17	17.5	15	4	I38336	hypothetical TBL/M
91	17	17.5	16	2	E41425	cytochrome P450 IF
92	17	17.5	16	2	A60551	leukocyte elastase
93	17	17.5	16	2	A44413	proteasome endopep
94	17	17.5	16	2	PH1771	T cell receptor al
95	17	17.5	16	2	E49255	T-cell receptor be
96	17	17.5	16	2	F49039	T-cell receptor be
97	17	17.5	16	2	H49039	T-cell receptor be
98	17	17.5	16	2	G24687	T-cell receptor be
99	17	17.5	16	2	PH0767	T-cell receptor be
100	17	17.5	17	2	PH1367	Ig heavy chain DJ

ALIGNMENTS

RESULT 1

PH1822
T cell receptor alpha chain V region (clone SPBL V alpha 24-5) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1822

R/Portcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1822

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 <POR>

A/Cross-references: UNIPARC:UPI000017C389

Query Match

Best Local Similarity 26.8%; Score 26; DB 2; Length 17;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PNHLSKIAP 11

Db 7 PNSSASKIIF 16

RESULT 2

S66458
ferredoxin - Rhizobium meliloti (fragment)

C/Species: Rhizobium meliloti

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C/Accession: S66458

R/Riedel, K.U.; Jouanneau, Y.; Masepohl, B.; Puehler, A.; Klipp, W.

A/Title: A Rhizobium meliloti ferredoxin (FdXn) purified from Escherichia coli donates e

A/Reference number: S66458; MUID:95377307; PMID:7649175

A/Accession: S66458

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <RIE>

A/Cross-references: UNIPARC:UPI000017A9D5

C/Genetics:

A/Gene: fdxN

Query Match

Best Local Similarity 25.8%; Score 25; DB 2; Length 10;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 AFKIVSQE 17

Db 1 AFKIIASQ 8

RESULT 3

S43321

RNA-binding protein - garden pea (fragment)

C/Species: Pisum sativum (garden pea)

C/Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C/Accession: S43321

R/Lakhani, S.; Khanna, N.C.; Tewari, K.K.

Plant Mol. Biol. 23, 963-979, 1993

A/Title: Nascent transcript-binding protein of the pea chloroplast transcriptionally act

A/Reference number: S43321; MUID:94083566; PMID:8260634

A/Accession: S43321

A/Molecule type: protein

A/Residues: 1-15 <LAK>

A/Cross-references: UNIPROT:Q9T2J9; UNIPARC:UPI000008D2B8

C/Function:

A/Description: probably involved in the transcription of chloroplast genes

C/Keywords: RNA binding

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 NHLNSKI 9

Db 2 NHINGTI 8

RESULT 4

A49018

myosin heavy chain, fast skeletal muscle type X - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999

C/Accession: A49018; S32161

R/DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Schiaffir

J. Cell Biol. 123, 823-835, 1993

A/Title: Type 2X-myosin heavy chain is coded by a muscle fiber type-specific and developm

A/Reference number: A49018; MUID:94043465; PMID:8227143

A/Accession: A49018

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-14 <DEN>

A/Cross-references: UNIPARC:UPI00000E6B5F; GB:X72591; NID:G288645; PIDN:CAA51189.1; PID:9

R/DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Merlie, J.; Buckingham, H.

submitted to the EMBL data Library, March 1993

A/Description: Type 2X myosin heavy chain is coded by a muscle fiber type-specific and d

A/Reference number: S32161

A/Accession: S32161

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-14 <DEN2>

A/Cross-references: UNIPARC:UPI00000E6B5F; EMBL:X72591; NID:G288645; PIDN:CAA51189.1; PI

C/Superfamily: myosin heavy chain; myosin motor domain homology

C/Keywords: skeletal muscle

Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 14;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 KIVSQE 17

Db 9 KIISEE 14

RESULT 5

PC2196

zymogen granule membrane associated protein, ZAP47 - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PC2196

R/Fukuoka, S.

Biosci. Biotechnol. Biochem. 58, 1282-1285, 1994

A/Title: Analysis of ZAPs, zymogen granule membrane associated proteins, in the regulate

A/Reference number: PC2195; MUID:94362286; PMID:7765250

A/Accession: PC2196

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <FUK>

A/Cross-references: UNIPARC:UPI000017C437

Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 17;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPNHIN 6

Db 5 DENHIN 10

RESULT 6

JP0073

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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:45:40 ; Search time 224 Seconds
(without alignments)
59.844 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLNSKIAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 12690

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	26.8	15	2	Q6GWV7 BOVIN
2	26	26.8	15	2	Q8C9M9 MOUSE
3	25	25.8	11	2	Q4X8K4 PLACH
4	25	25.8	15	2	Q679L5 HUMAN
5	25	25.8	15	2	Q9UMY6 HUMAN
6	25	25.8	15	2	Q9TJ29 PEA
7	25	25.8	16	2	Q8WXZ7 HUMAN
8	25	25.8	16	2	Q5C2N5 SCHUA
9	25	25.8	16	2	Q7RPN7 PLAYO
10	25	25.8	17	2	Q5J747 COXBU
11	25	25.8	18	2	Q43834 HUMAN
12	25	25.8	18	2	Q5C4J8 SCHUA
13	24	24.7	9	2	Q6EX64 PLACH
14	24	24.7	10	2	Q9R5N4 CLOBO
15	24	24.7	13	1	PROFX ORYSA
16	24	24.7	16	1	FORM1 MYRGU
17	24	24.7	16	1	FORM2 MYRGU
18	24	24.7	19	2	Q5C5Q4 SCHUA
19	24	24.7	19	2	Q4XAG4 PLACH
20	24	24.7	19	2	Q36925 NICPL
21	24	24.7	19	2	Q7GFF1 NICOTIANA V
22	24	24.7	19	2	Q7GFF2 SOLA
23	24	24.7	19	2	Q9G466 BRAJU
24	23	23.7	10	2	Q4Z638 PLACH
25	23	23.7	12	2	Q8MJEA AOTAZ
26	23	23.7	13	2	Q957T7 9PERC
27	23	23.7	14	2	Q06415 RATRAT
28	23	23.7	15	2	Q8ST73 DROPS
29	23	23.7	15	2	Q4XBA3 PLACH
30	23	23.7	15	2	Q9TR17 RABIT
31	23	23.7	16	2	Q7S0C4 NEUR

Q4Y777	PLACH	17	2	Q4Y777	PLACH
Q4YDE5	PLABE	17	2	Q4YDE5	PLABE
Q9T2S0	SOLTU	17	2	Q9T2S0	SOLTU
Q9TR05	BOVIN	18	2	Q9TR05	BOVIN
Q6VPR3	POKXV	18	2	Q6VPR3	POKXV
Q4XV14	PLACH	19	2	Q4XV14	PLACH
Q9S8Q0	PINSY	19	2	Q9S8Q0	PINSY
Q70YA2	9LAMI	9	2	Q70YA2	9LAMI
Q7M117	LEUME	9	2	Q7M117	LEUME
Q9R5N6	CLOBO	10	2	Q9R5N6	CLOBO
P89269	GVXN	11	2	P89269	GVXN
Q9R5N5	CLOBO	13	2	Q9R5N5	CLOBO
P80621	zea mays (m	14	1	UC15	MAIZE
Q06414	rattus ratt	14	2	Q06414	RATRT
Q9QVF3	rattus sp.	14	2	Q9QVF3	9MURI
P84026	bothrops ja	15	1	THBI	BOTJA
Q9QV62	mus sp. dif	15	2	Q9QV62	9MURI
P63181	sus scrofa	16	1	CBLN1	PIG
P63182	rattus norv	16	1	CBLN1	RAT
Q9TZR2	hallois ru	16	2	Q9TZR2	HALRU
Q4XEW2	PLACH	16	2	Q4XEW2	PLACH
Q5OG96	TRASP	16	2	Q5OG96	TRASP
Q5OG97	TRASP	16	2	Q5OG97	TRASP
Q5OG99	TRAGELAPHUS	16	2	Q5OG99	TRAGELAPHUS
Q5OGA1	TRAGELAPHUS	16	2	Q5OGA1	9CBTA
Q5OGA3	TRAGELAPHUS	16	2	Q5OGA3	TRAAN
Q5OGA4	TRAIM	16	2	Q5OGA4	TRAIM
Q5OGA6	TRAST	16	2	Q5OGA6	TRAST
Q5OGA8	TRAOR	16	2	Q5OGA8	TRAOR
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Q8N6B0	HUMAN	17	2	Q8N6B0	HUMAN
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Q9SMV5	RAPME	18	2	Q9SMV5	RAPME
Q9SMV6	RAPSH	18	2	Q9SMV6	RAPSH
Q9SMV7	RAPCA	18	2	Q9SMV7	RAPCA
Q9SMV8	LITWA	18	2	Q9SMV8	LITWA
Q9SMV9	ANTMR	18	2	Q9SMV9	ANTMR
Q9SMW0	PELCP	18	2	Q9SMW0	PELCP
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Q9SMW3	REDFU	18	2	Q9SMW3	REDFU
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Q9SMW5	ALCBU	18	2	Q9SMW5	ALCBU
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Q9SMX0	TRAOR	18	2	Q9SMX0	TRAOR
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Q9UCG3	HUMAN	19	2	Q9UCG3	HUMAN
Q9TWK8	9TRYP	19	2	Q9TWK8	9TRYP
Q82685	GERRY	19	2	Q82685	GERRY
Q9YQW7	9GBMI	19	2	Q9YQW7	9GBMI
Q5UIW1	GRAVE	19	2	Q5UIW1	GRAVE
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1	DYS3	21	1	DYS3	LIMTE
1	Q8R2F6	21	1	Q8R2F6	RAT
1	FARB	21	1	FARB	ASCUS
1	Q9UM46	21	1	Q9UM46	HUMAN
1	Q71UL1	21	1	Q71UL1	HALRU

ALIGNMENTS


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RESULT 1
Q6GW7_BOVIN PRELIMINARY; PRT; 15 AA.
AC Q6GW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 8 (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Meade K.G., Fitzgerald D.C., Murphy E.P., Baird A.W., MacHugh D.B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY627308; AAT47550.1; -; Genomic_DNA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1504 MW; DA1932E93C487C14 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 5; Gaps 0;

QY 5 LNSKIAFKIVQBP 19
DB 1 MTSKLAVALLAAPPA 15

RESULT 2
Q8C9M9_MOUSE PRELIMINARY; PRT; 15 AA.
AC Q8C9M9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630035G04 product:DEAD/H (Asp-Glu-Ala-Asp/His) box
DE polypeptide 26, full insert sequence. (fragment).
GN Dmdx26;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staublel P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Brownstein N.J., Bult C., Fletcher C., Fujita P., Gariboldi M.F.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK041758; BAC31055.1; -; mRNA.
DR MGI; MGI:1202397; Ddx26.
DR GO; GO:0005615; C:extracellular space; TAS.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1816 MW; CDF3F69D90D63857 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NHLNS 7
DB 10 NHINS 14

RESULT 3
Q4X8K4_PLACH PRELIMINARY; PRT; 11 AA.
AC Q4X8K4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:48:51 ; Search time 47 Seconds
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Title: US-10-799-005a-1

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 213352

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	73.2	15	US-08-787-547-24	Sequence 24, Appl
2	71	73.2	15	US-08-400-796-3	Sequence 3, Appl
3	31	32.0	12	US-08-637-759B-448	Sequence 448, Appl
4	31	32.0	12	US-08-871-355A-448	Sequence 448, Appl
5	31	32.0	12	US-09-201-945-448	Sequence 448, Appl
6	31	32.0	17	US-08-239-854-6	Sequence 6, Appl
7	30	30.9	17	US-08-160-604-62	Sequence 62, Appl
8	29	29.9	15	US-09-009-953-76	Sequence 76, Appl
9	28	28.9	18	US-09-268-480-21	Sequence 21, Appl
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14	27	27.8	13	US-10-729-121-5	Sequence 5, Appl
15	27	27.8	19	US-09-442-989-30	Sequence 30, Appl
16	26	26.8	9	US-09-518-046-101	Sequence 101, Appl
17	26	26.8	9	US-09-650-371-101	Sequence 101, Appl
18	26	26.8	15	US-08-204-658B-16	Sequence 16, Appl
19	26	26.8	15	US-08-470-702-16	Sequence 16, Appl
20	26	26.8	15	US-08-467-831-16	Sequence 16, Appl
21	26	26.8	17	US-10-204-664A-3	Sequence 3, Appl
22	26	26.8	17	US-09-864-675-17	Sequence 17, Appl
23	26	26.8	19	US-09-308-935-15	Sequence 15, Appl
24	25	25.8	9	US-09-841-808-10	Sequence 10, Appl
25	25	25.8	10	US-09-490-702B-57	Sequence 57, Appl
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27	25	25.8	10	US-09-935-430-292	Sequence 292, Appl

28	25	25.8	10	US-09-935-430-363	Sequence 363, App
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52	25	25.8	15	US-09-009-953-224	Sequence 224, App
53	25	25.8	15	US-09-311-784A-418	Sequence 418, App
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56	25	25.8	15	PCT-US94-07902-5	Sequence 5, Appl
57	25	25.8	16	US-07-752-101A-15	Sequence 15, Appl
58	25	25.8	16	US-09-456-399-11	Sequence 11, Appl
59	25	25.8	16	US-09-489-847-302	Sequence 102, App
60	25	25.8	17	US-08-497-599-2	Sequence 2, Appl
61	25	25.8	17	US-08-497-599-18	Sequence 18, Appl
62	25	25.8	17	US-09-009-953-273	Sequence 273, App
63	25	25.8	17	US-09-311-784A-417	Sequence 417, App
64	25	25.8	18	US-08-342-449-10	Sequence 10, Appl
65	25	25.8	18	US-08-630-916A-104	Sequence 104, App
66	25	25.8	18	US-08-630-915A-160	Sequence 160, App
67	25	25.8	18	US-09-311-784A-416	Sequence 416, App
68	25	25.8	18	US-09-879-957-160	Sequence 160, App
69	24	24.7	8	US-08-335-7330-32	Sequence 32, Appl
70	24	24.7	9	US-08-669-656A-20	Sequence 20, Appl
71	24	24.7	9	US-08-475-955-44	Sequence 44, Appl
72	24	24.7	9	US-07-867-819D-44	Sequence 44, Appl
73	24	24.7	10	US-09-256-194-7	Sequence 7, Appl
74	24	24.7	10	US-09-434-476A-11	Sequence 11, Appl
75	24	24.7	10	US-09-490-702B-60	Sequence 60, Appl
76	24	24.7	10	US-09-767-460-60	Sequence 60, Appl
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85	24	24.7	15	US-08-592-646A-52	Sequence 52, Appl
86	24	24.7	15	US-08-462-507A-82	Sequence 82, Appl
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89	24	24.7	15	US-09-165-423-52	Sequence 52, Appl
90	24	24.7	15	US-09-009-953-270	Sequence 270, App
91	24	24.7	15	US-10-059-506-15	Sequence 15, Appl
92	24	24.7	15	US-10-012-896-966	Sequence 966, App
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94	24	24.7	17	US-09-518-036-22	Sequence 22, Appl
95	24	24.7	17	US-10-279-130-22	Sequence 22, Appl
96	23	23.7	6	US-08-900-241-63	Sequence 63, Appl
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98	23	23.7	10	US-08-159-339A-574	Sequence 574, App
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100	23	23.7	10	US-09-767-460-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-787-547-24
; Sequence 24, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-24

Query Match 73.2%; Score 71; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAPKIVSQEPA 19
Db 1 LNSKIAPKIVSQEPA 15
|||||

RESULT 2
US-08-400-796-3
; Sequence 3, Application US/08400796
; Patent No. 5874531
; GENERAL INFORMATION:
; APPLICANT: STROMINGER, JACK L.
; APPLICANT: WUCHERPFENNIG, KAI
; TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
; TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE

CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,796
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: H0498/7015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
US-08-400-796-3

Query Match 73.2%; Score 71; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAPKIVSQEPA 19
Db 1 LNSKIAPKIVSQEPA 15
|||||

RESULT 3
US-08-637-7598-448
; Sequence 448, Application US/086377598
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,7598
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:56:01 ; Search time 160 Seconds
(without alignments)
49.617 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLNKTAFKIVSQEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 364077

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	19	5	US-10-799-005A-1
2	71	73.2	15	3	US-09-909-460-24
3	71	73.2	15	3	US-09-872-836-24
4	71	73.2	15	3	US-09-906-206A-30
5	71	73.2	15	5	US-10-758-970-24
6	31	32.0	15	5	US-10-454-246-122
7	31	32.0	16	5	US-10-454-246-120
8	30.5	31.4	19	4	US-10-153-344-10
9	29	29.9	11	4	US-10-466-466-4
10	29	29.9	15	4	US-10-103-395-76
11	29	29.9	15	4	US-10-186-867-30
12	29	29.9	16	4	US-10-225-567A-1162
13	29	29.9	17	5	US-10-488-528-14
14	29	29.9	18	4	US-10-029-386-33316
15	28	28.9	18	4	US-10-043-487-406
16	28	28.9	18	4	US-10-244-488-21
17	28	28.9	18	4	US-10-244-488-28
18	28	28.9	19	3	US-09-864-761-44631
19	28	28.9	19	6	US-11-111-953-218
20	27	27.8	6	5	US-10-799-005A-2
21	27	27.8	6	5	US-10-799-005A-3
22	27	27.8	12	5	US-10-860-050-586
23	27	27.8	13	6	US-11-077-752-5
24	27	27.8	14	4	US-10-712-425-1268
25	27	27.8	14	5	US-10-773-032-1268
26	27	27.8	17	3	US-09-946-175-6
27	26	26.8	9	4	US-10-357-175-101

28	26.8	9	4	US-10-455-720-101	Sequence 101, App
29	26.8	9	4	US-10-334-726-187	Sequence 187, App
30	26.8	9	4	US-10-024-652-40	Sequence 40, Appl
31	26.8	9	4	US-10-024-652-601	Sequence 601, App
32	26.8	9	4	US-10-024-652-894	Sequence 894, App
33	26.8	9	4	US-10-024-652-983	Sequence 983, App
34	26.8	9	4	US-10-024-652-1068	Sequence 1068, App
35	26.8	9	4	US-10-024-652-1391	Sequence 1391, App
36	26.8	9	4	US-10-024-652-1437	Sequence 1437, App
37	26.8	9	4	US-10-024-652-1470	Sequence 1470, App
38	26.8	10	4	US-10-024-652-63	Sequence 63, Appl
39	26.8	10	4	US-10-024-652-65	Sequence 65, Appl
40	26.8	10	4	US-10-024-652-200	Sequence 200, App
41	26.8	10	4	US-10-024-652-274	Sequence 274, App
42	26.8	10	4	US-10-024-652-372	Sequence 372, App
43	26.8	10	4	US-10-024-652-569	Sequence 569, App
44	26.8	10	4	US-10-024-652-660	Sequence 660, App
45	26.8	10	4	US-10-024-652-686	Sequence 686, App
46	26.8	10	4	US-10-024-652-1552	Sequence 1552, App
47	26.8	10	4	US-10-024-652-1618	Sequence 1618, App
48	26.8	10	4	US-10-024-652-1619	Sequence 1619, App
49	26.8	10	4	US-10-024-652-1701	Sequence 1701, App
50	26.8	10	4	US-10-024-652-1709	Sequence 1709, App
51	26.8	10	4	US-10-024-652-1730	Sequence 1730, App
52	26.8	10	4	US-10-024-652-1818	Sequence 1818, App
53	26.8	10	4	US-10-024-652-1896	Sequence 1896, App
54	26.8	10	4	US-10-024-652-1904	Sequence 1904, App
55	26.8	11	3	US-09-795-008A-137	Sequence 137, App
56	26.8	12	4	US-10-286-457-34	Sequence 34, Appl
57	26.8	13	4	US-10-403-980-27	Sequence 27, Appl
58	26.8	14	4	US-10-417-895A-33	Sequence 33, Appl
59	26.8	15	4	US-10-024-652-2093	Sequence 2093, App
60	26.8	15	4	US-10-024-652-2158	Sequence 2158, App
61	26.8	15	4	US-10-024-652-2175	Sequence 2175, App
62	26.8	15	4	US-10-024-652-2199	Sequence 2199, App
63	26.8	15	4	US-10-024-652-2203	Sequence 2203, App
64	26.8	15	4	US-10-024-652-2218	Sequence 2218, App
65	26.8	15	4	US-10-024-652-2231	Sequence 2231, App
66	26.8	15	4	US-10-024-652-2282	Sequence 2282, App
67	26.8	15	4	US-10-024-652-2341	Sequence 2341, App
68	26.8	15	4	US-10-024-652-2342	Sequence 2342, App
69	26.8	15	4	US-10-024-652-2424	Sequence 2424, App
70	26.8	15	4	US-10-024-652-2425	Sequence 2425, App
71	26.8	15	4	US-10-024-652-2426	Sequence 2426, App
72	26.8	15	4	US-10-024-652-2463	Sequence 2463, App
73	26.8	15	4	US-10-024-652-2517	Sequence 2517, App
74	26.8	15	4	US-10-024-652-2518	Sequence 2518, App
75	26.8	16	3	US-09-791-378-550	Sequence 550, App
76	26.8	16	3	US-09-791-378-564	Sequence 564, App
77	26.8	16	3	US-09-791-393-238	Sequence 238, App
78	26.8	16	3	US-09-791-389-238	Sequence 238, App
79	26.8	16	3	US-09-791-377-550	Sequence 550, App
80	26.8	16	3	US-09-791-377-564	Sequence 564, App
81	26.8	16	4	US-10-076-047A-27	Sequence 27, Appl
82	26.8	16	4	US-10-076-047A-49	Sequence 49, Appl
83	26.8	16	4	US-10-220-481-82	Sequence 82, Appl
84	26.8	17	3	US-09-864-675-17	Sequence 17, Appl
85	26.8	17	4	US-10-133-210-261	Sequence 261, App
86	26.8	17	4	US-10-147-910-5	Sequence 5, Appl
87	26.8	17	4	US-10-239-313A-293	Sequence 293, App
88	26.8	19	3	US-09-900-147-15	Sequence 15, Appl
89	26.8	19	6	US-11-008-653-152	Sequence 152, App
90	25.8	9	5	US-10-825-026-65	Sequence 65, Appl
91	25.8	10	2	US-08-344-824-380	Sequence 380, App
92	25.8	10	3	US-09-767-460-57	Sequence 57, Appl
93	25.8	10	3	US-09-935-430-62	Sequence 62, Appl
94	25.8	10	3	US-09-935-430-292	Sequence 292, App
95	25.8	10	3	US-09-935-430-363	Sequence 363, App
96	25.8	10	3	US-09-935-430-502	Sequence 502, App
97	25.8	10	3	US-09-935-430-608	Sequence 608, App
98	25.8	10	4	US-10-062-710-201	Sequence 201, App
99	25.8	10	4	US-10-277-292-62	Sequence 62, Appl
100	25.8	10	4	US-10-277-292-292	Sequence 292, App

ALIGNMENTS

RESULT 1
US-10-799-005A-1
; Sequence 1, Application US/10799005A
; Publication No. US2005020234A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, James
; APPLICANT: Yu, Bei
; TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
; FILE REFERENCE: PEPT-005
; CURRENT APPLICATION NUMBER: US/10/799,005A
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from human desmoglein 3
; OTHER INFORMATION: protein
US-10-799-005A-1

Query Match 100.0%; Score 97; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPNHLSKIAFKIVSQEPA 19
Db 1 EPNHLSKIAFKIVSQEPA 19
|||||

RESULT 2
US-09-909-460-24
; Sequence 24, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-24

Query Match 73.2%; Score 71; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAFKIVSQEPA 19
Db 1 LNSKIAFKIVSQEPA 15
|||||

RESULT 3
US-09-872-836-24
; Sequence 24, Application US/09872836
; Publication No. US20040142475A1

; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-24

Query Match 73.2%; Score 71; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAFKIVSQEPA 19
Db 1 LNSKIAFKIVSQEPA 15
|||||

RESULT 4
US-09-906-206A-30
; Sequence 30, Application US/09906206A
; Publication No. US20050239170A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Aziz, Nazneen
; APPLICANT: Chen, Hongmin
; APPLICANT: Stenad-Moghadam, Bijan
; APPLICANT: Yin, Peng
; TITLE OF INVENTION: ALPHA-MSH RELATED COMPOUNDS AND METHODS
; FILE REFERENCE: 08191-015001
; CURRENT APPLICATION NUMBER: US/09/906,206A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 60/218,381
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/226,382
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/238,380
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/258,764
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: US 60/298,317
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-206A-30

Query Match 73.2%; Score 71; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNSKIAFKIVSQEPA 19
Db 1 LNSKIAFKIVSQEPA 15
|||||

RESULT 5
US-10-758-970-24
; Sequence 24, Application US/10758970

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 01:56:42 ; Search time 9 Seconds

(without alignments)
6.399 Million cell updates/sec

Title: US-10-799-005A-1

Perfect score: 97

Sequence: 1 EPNHLNSKIAFKIVSOEPA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 6009

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdb:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	27.8	14	1 US-10-989-226-1	Sequence 1, Appli
2	27	27.8	19	1 US-10-503-575-117	Sequence 117, App
3	23	23.7	13	1 US-10-511-559-530	Sequence 530, App
4	23	23.7	13	1 US-10-511-559-531	Sequence 531, App
5	23	23.7	13	1 US-10-511-559-532	Sequence 532, App
6	23	23.7	13	1 US-10-511-559-533	Sequence 533, App
7	23	23.7	13	1 US-10-511-559-535	Sequence 535, App
8	23	23.7	19	1 US-10-503-575-310	Sequence 310, App
9	22	22.7	16	7 US-11-054-515-2764	Sequence 2764, Ap
10	22	22.7	17	1 US-10-723-207-79	Sequence 79, Appl
11	22	22.7	17	1 US-10-723-207-86	Sequence 86, Appl
12	22	22.7	19	1 US-10-503-575-135	Sequence 135, App
13	21	21.6	10	1 US-10-502-535A-45	Sequence 45, Appl
14	21	21.6	10	7 US-11-011-666-3	Sequence 3, Appli
15	21	21.6	10	7 US-11-021-441-99	Sequence 99, Appl
16	21	21.6	10	7 US-11-558-848-39	Sequence 39, Appl
17	21	21.6	11	1 US-10-484-271A-2	Sequence 2, Appli
18	21	21.6	13	1 US-10-511-559-451	Sequence 451, App
19	21	21.6	13	1 US-10-511-559-452	Sequence 452, App
20	21	21.6	13	1 US-10-511-559-453	Sequence 453, App
21	21	21.6	13	1 US-10-511-559-454	Sequence 454, App
22	21	21.6	13	1 US-10-511-559-516	Sequence 516, App
23	21	21.6	14	1 US-10-512-184-45	Sequence 45, Appl
24	21	21.6	14	1 US-10-925-970-14	Sequence 14, Appl
25	21	21.6	14	7 US-11-040-159-123	Sequence 123, App

26	21	21.6	14	7 US-11-054-515-2652	Sequence 2652, Ap
27	21	21.6	14	7 US-11-054-515-2661	Sequence 2661, Ap
28	21	21.6	14	7 US-11-054-515-2663	Sequence 2663, Ap
29	21	21.6	14	7 US-11-054-515-2665	Sequence 2665, Ap
30	21	21.6	15	1 US-10-989-226-16	Sequence 16, Appl
31	21	21.6	15	7 US-11-054-515-2765	Sequence 2765, Ap
32	21	21.6	16	7 US-11-054-515-3022	Sequence 3022, Ap
33	21	21.6	17	7 US-11-090-908-6	Sequence 6, Appli
34	21	21.6	19	1 US-10-503-575-178	Sequence 178, App
35	21	21.6	19	1 US-10-503-575-174	Sequence 174, App
36	21	21.6	19	1 US-10-503-575-245	Sequence 245, App
37	21	21.6	19	1 US-10-503-575-246	Sequence 246, App
38	20	20.6	12	1 US-10-503-575-73	Sequence 73, Appl
39	20	20.6	12	7 US-11-016-706-24	Sequence 24, Appl
40	20	20.6	13	1 US-10-966-648-12	Sequence 12, Appl
41	20	20.6	13	1 US-10-511-559-515	Sequence 515, App
42	20	20.6	13	1 US-10-511-559-737	Sequence 737, App
43	20	20.6	13	1 US-10-511-559-837	Sequence 837, App
44	20	20.6	13	1 US-10-511-559-838	Sequence 838, App
45	20	20.6	13	1 US-10-511-559-839	Sequence 839, App
46	20	20.6	13	1 US-10-511-559-840	Sequence 840, App
47	20	20.6	13	1 US-10-511-559-841	Sequence 841, App
48	20	20.6	13	1 US-10-511-559-842	Sequence 842, App
49	20	20.6	15	7 US-11-022-562-38	Sequence 38, Appl
50	20	20.6	16	7 US-11-089-764-1	Sequence 1, Appli
51	20	20.6	16	7 US-11-089-764-43	Sequence 43, Appl
52	20	20.6	17	1 US-10-503-575-87	Sequence 87, Appl
53	20	20.6	17	7 US-11-038-501-10	Sequence 10, Appl
54	20	20.6	17	7 US-11-059-633-13	Sequence 13, Appl
55	20	20.6	18	1 US-10-503-575-77	Sequence 77, Appl
56	20	20.6	19	1 US-10-503-575-106	Sequence 106, App
57	20	20.6	19	1 US-10-503-575-151	Sequence 151, App
58	20	20.6	19	1 US-10-503-575-221	Sequence 221, App
59	20	20.6	19	1 US-10-503-575-252	Sequence 252, App
60	20	20.6	19	1 US-10-503-575-258	Sequence 258, App
61	20	20.6	19	1 US-10-503-575-264	Sequence 264, App
62	19	19.6	9	1 US-10-969-314-30	Sequence 30, Appl
63	19	19.6	9	7 US-11-010-748A-292	Sequence 292, App
64	19	19.6	9	7 US-11-033-365-101	Sequence 101, App
65	19	19.6	9	7 US-11-033-365-103	Sequence 103, App
66	19	19.6	11	7 US-11-010-748A-288	Sequence 288, App
67	19	19.6	13	1 US-10-511-559-450	Sequence 450, App
68	19	19.6	13	1 US-10-511-559-466	Sequence 466, App
69	19	19.6	13	1 US-10-511-559-467	Sequence 467, App
70	19	19.6	13	1 US-10-511-559-468	Sequence 468, App
71	19	19.6	13	1 US-10-511-559-555	Sequence 555, App
72	19	19.6	13	1 US-10-511-559-556	Sequence 556, App
73	19	19.6	13	1 US-10-511-559-760	Sequence 760, App
74	19	19.6	13	1 US-10-511-559-761	Sequence 761, App
75	19	19.6	13	1 US-10-511-559-762	Sequence 762, App
76	19	19.6	13	1 US-10-511-559-763	Sequence 763, App
77	19	19.6	13	1 US-10-511-559-764	Sequence 764, App
78	19	19.6	13	1 US-10-511-559-769	Sequence 769, App
79	19	19.6	13	1 US-10-511-559-770	Sequence 770, App
80	19	19.6	13	1 US-10-511-559-771	Sequence 771, App
81	19	19.6	13	1 US-10-511-559-772	Sequence 772, App
82	19	19.6	13	1 US-10-511-559-773	Sequence 773, App
83	19	19.6	13	1 US-10-511-559-774	Sequence 774, App
84	19	19.6	13	1 US-10-511-559-775	Sequence 775, App
85	19	19.6	13	1 US-10-511-559-795	Sequence 795, App
86	19	19.6	13	1 US-10-511-559-796	Sequence 796, App
87	19	19.6	15	1 US-10-614-599-19	Sequence 19, Appl
88	19	19.6	17	7 US-11-033-365-176	Sequence 176, App
89	19	19.6	17	7 US-11-033-365-177	Sequence 177, App
90	19	19.6	18	1 US-10-939-890-123	Sequence 123, App
91	19	19.6	18	7 US-11-092-496-14	Sequence 14, Appl
92	19	19.6	19	1 US-10-503-575-330	Sequence 330, App
93	18	18.6	4	7 US-11-011-666-14	Sequence 14, Appl
94	18	18.6	13	1 US-10-939-890-187	Sequence 187, App
95	18	18.6	13	1 US-10-511-559-99	Sequence 99, Appl
96	18	18.6	13	1 US-10-511-559-100	Sequence 100, App
97	18	18.6	13	1 US-10-511-559-101	Sequence 101, App
98	18	18.6	13	1 US-10-511-559-534	Sequence 534, App

99 18 18.6 13 1 US-10-511-559-778 Sequence 778, App
100 18 18.6 13 1 US-10-511-559-779 Sequence 779, App

ALIGNMENTS

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RESULT 1
US-10-989-226-1
; Sequence 1, Application US/10989226
; Publication No. US20050255491A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Xun
; APPLICANT: Afeyan, Noubar B.
; APPLICANT: Gordon, Neal F.
; TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: EPTM-P01-005
; CURRENT APPLICATION NUMBER: US/10/989,226
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,530
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/532,687
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide binding anti-p24 (HIV-1) antibody CB4-1
US-10-989-226-1

Query Match 27.8%; Score 27; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 9.1;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNHLSKIA 10
DB 4 PEDLNQKLA 12

RESULT 2
US-10-503-575-117
; Sequence 117, Application US/10503575
; Publication No. US2005024823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-117

Query Match 27.8%; Score 27; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 12 KIVSQEPA 19
DB 6 EVVSQTEPA 13

RESULT 3
US-10-511-559-530
; Sequence 530, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 530
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-530

Query Match 23.7%; Score 23; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 NHLNSK 8
DB 8 NHMSNK 13

RESULT 4
US-10-511-559-531
; Sequence 531, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 531
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-531

Query Match 23.7%; Score 23; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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